A

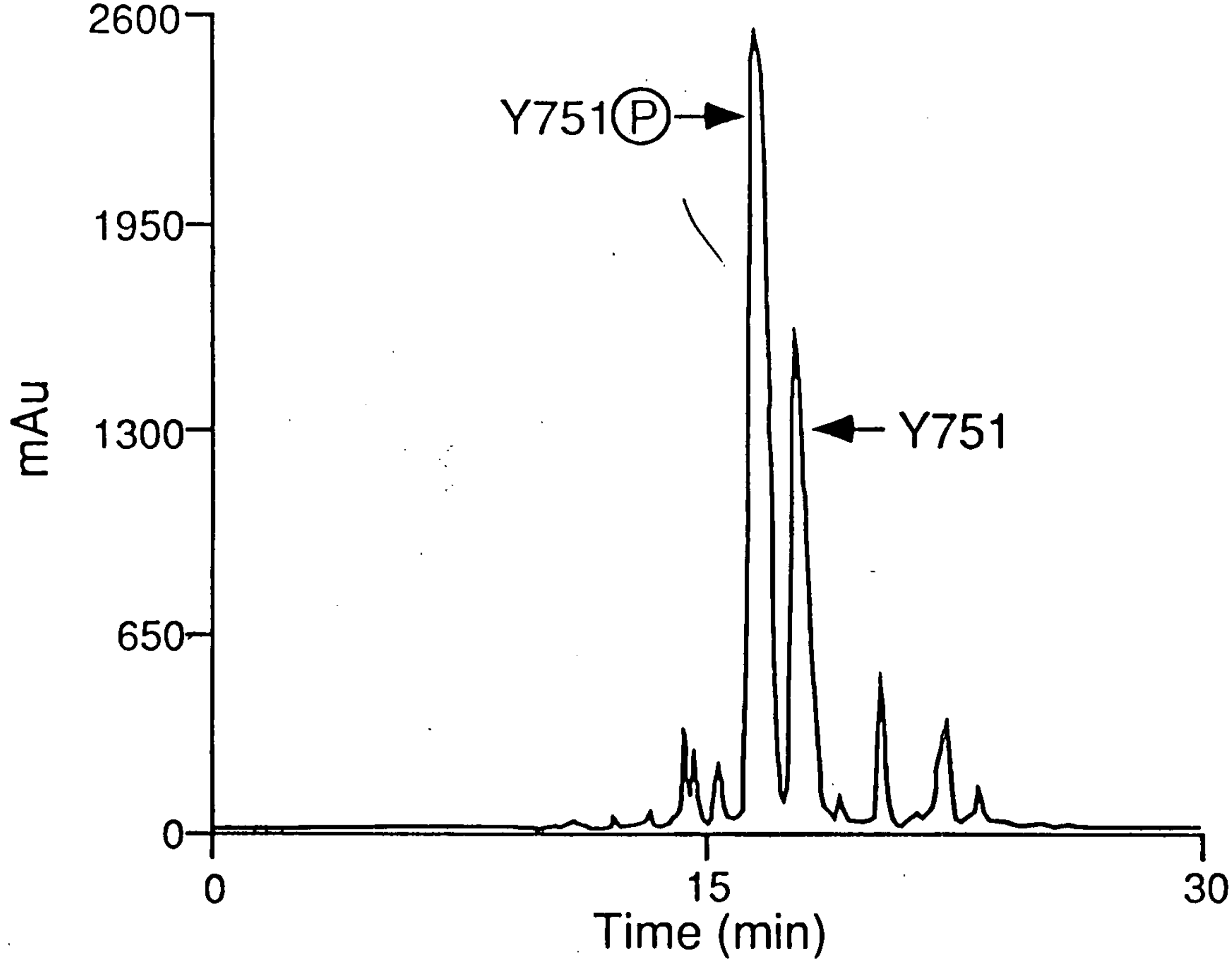


Figure 1

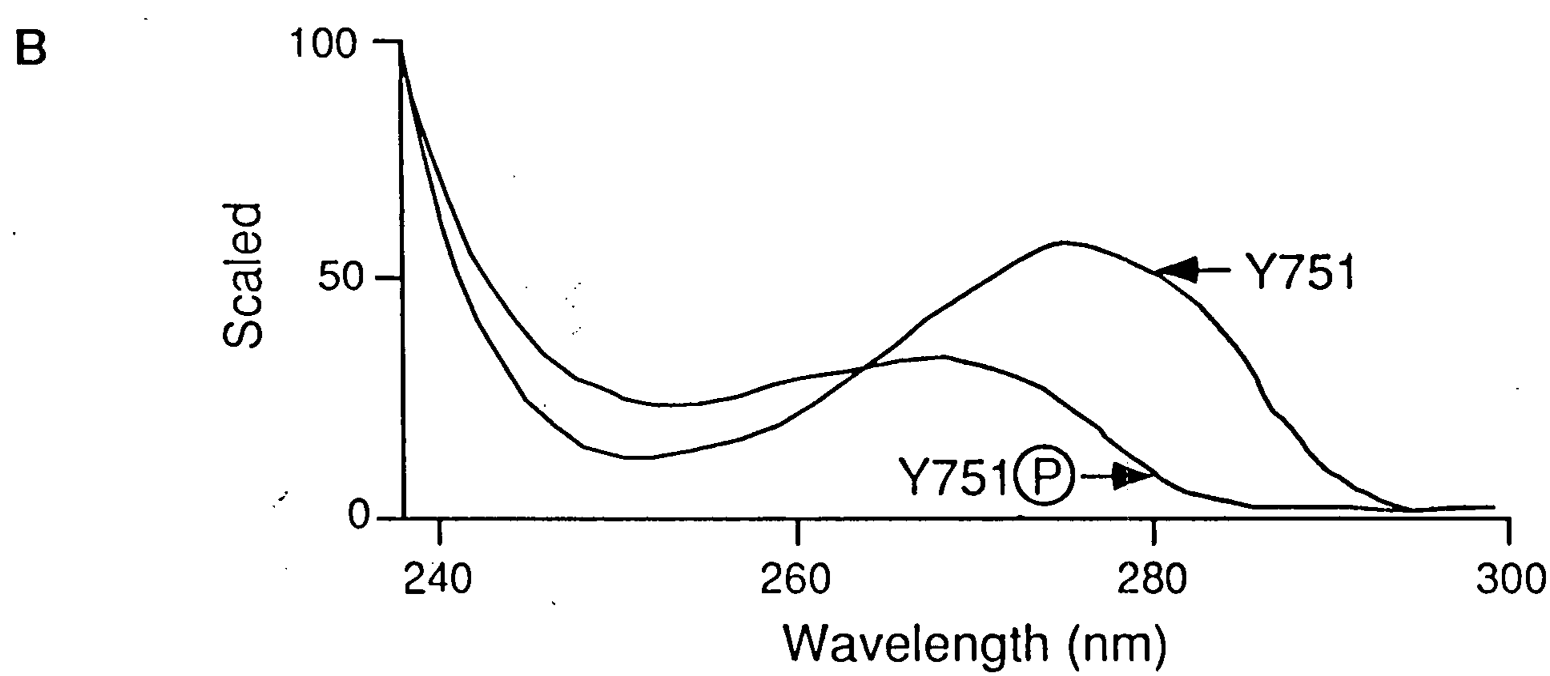


FIG 1 (contd)

C

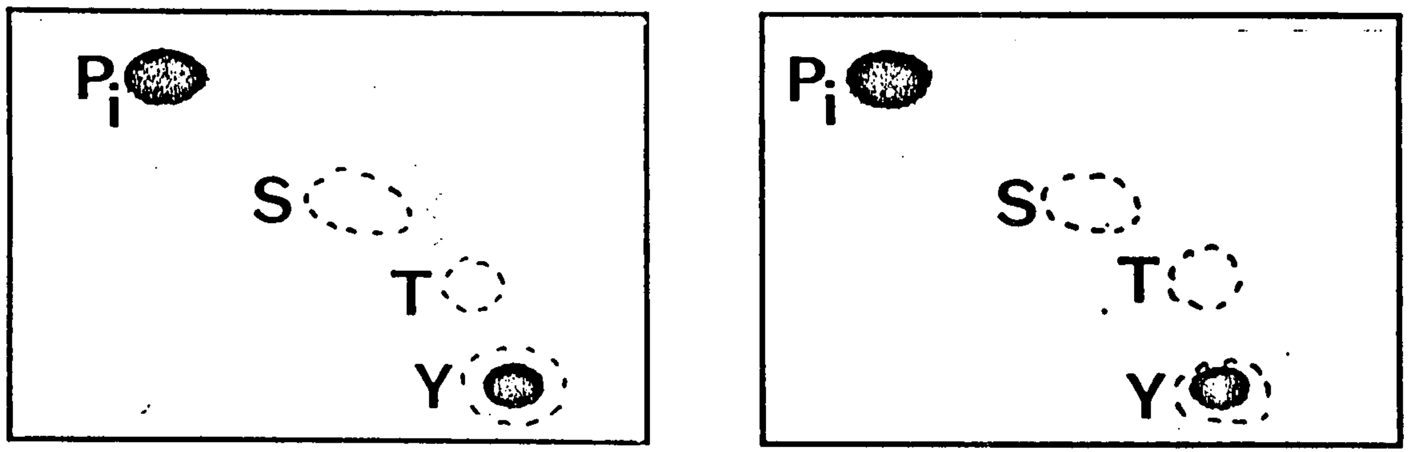


FIG 1 (contd)

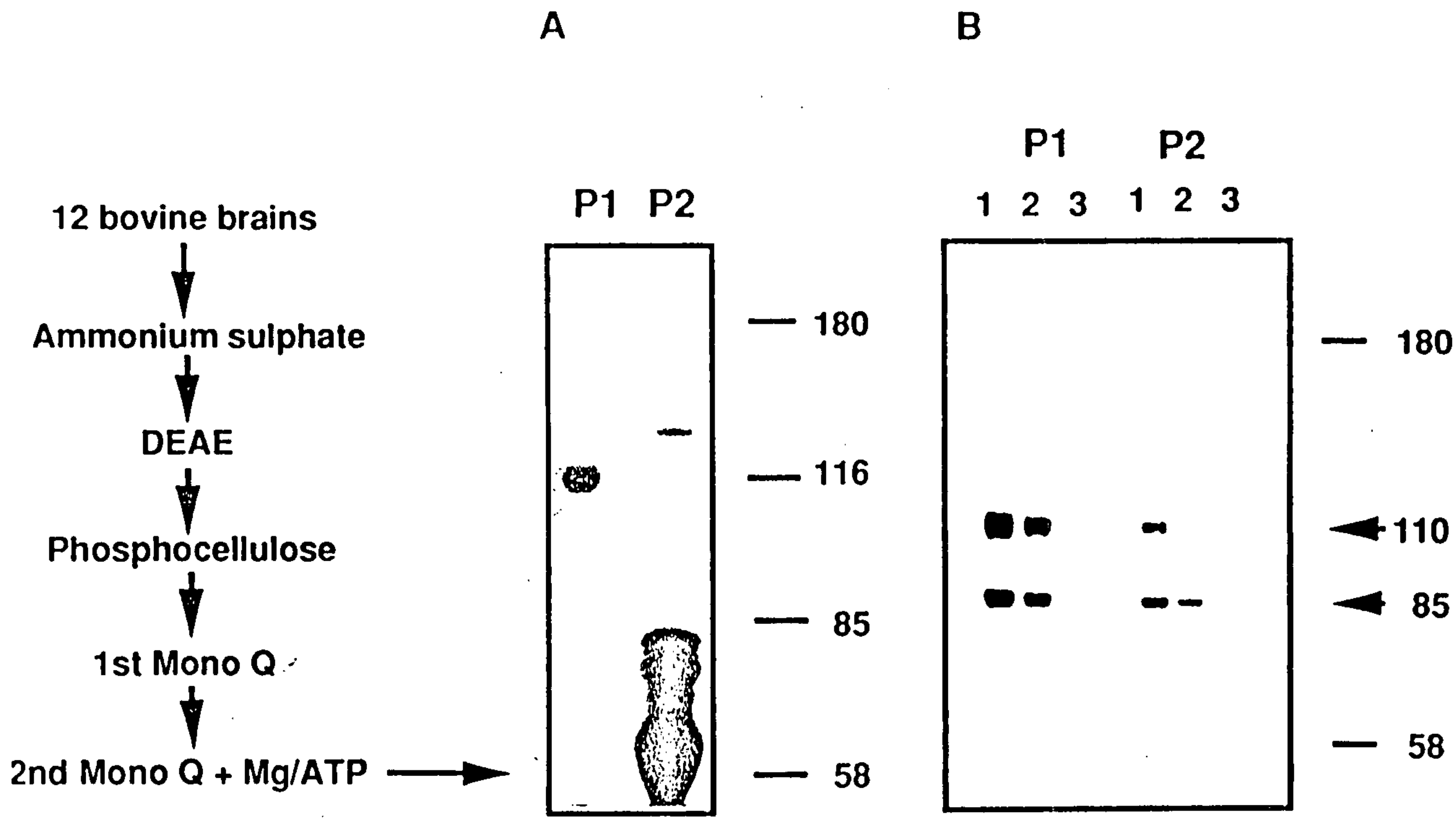

A
B
12 bovine brains
Ammonium sulphate
DEAE
Phosphocellulose
1st Mono Q
2nd Mono Q + Mg/ATP
P1 P2
180
116
85
58
P1
P2
1 2 3 1 2 3
180
110
85
58

Figure 2

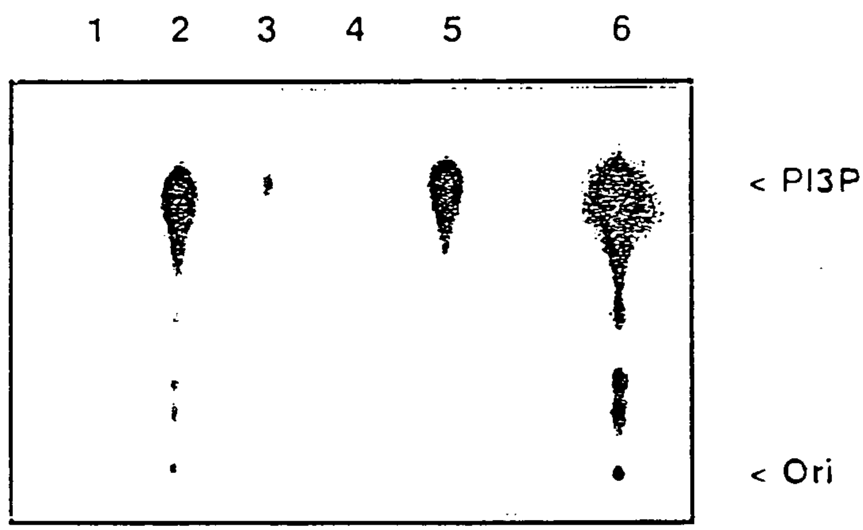
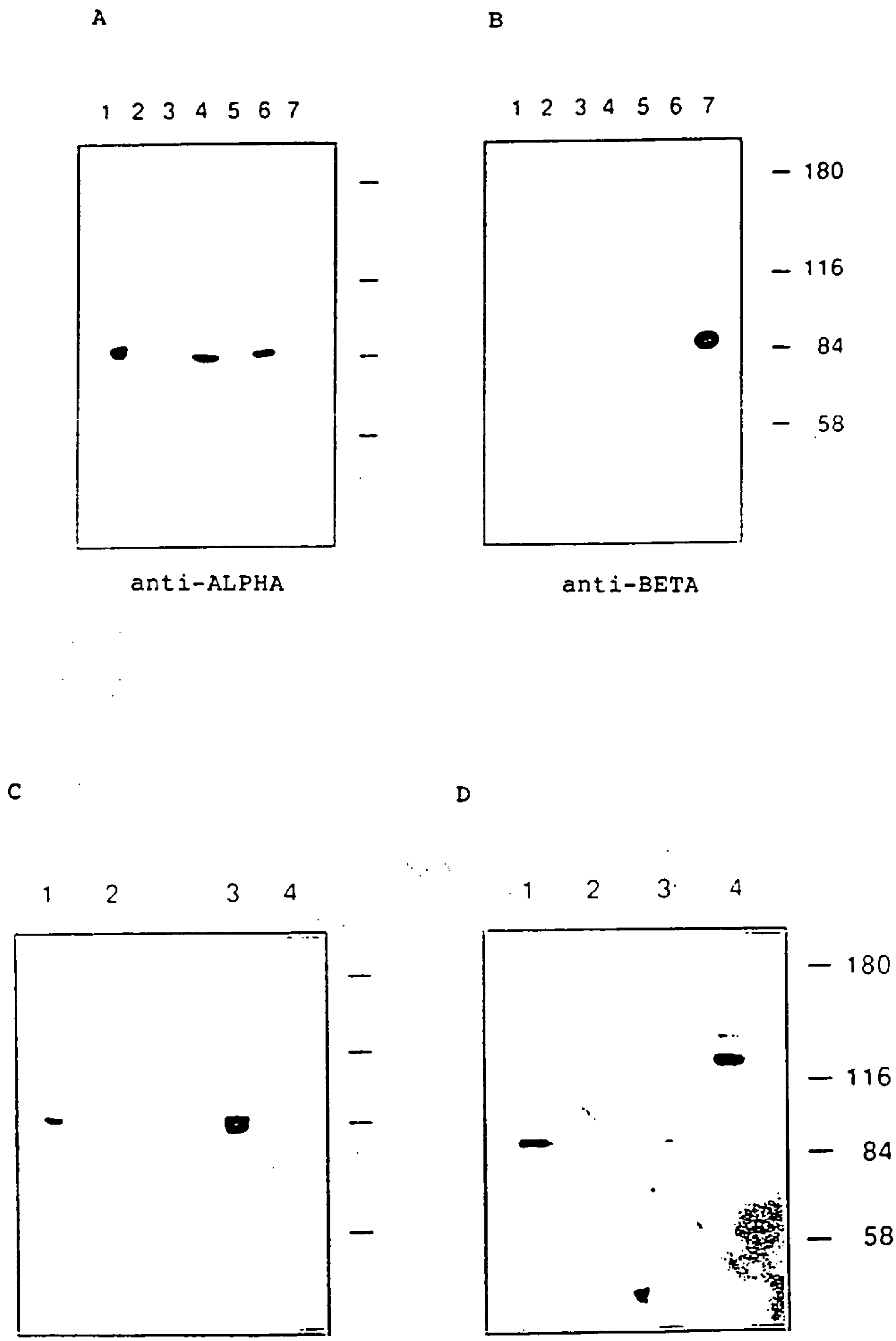


Figure 3

Figure 4


A
B
1 2 3 4 5 6 7
1 2 3 4 5 6 7
180
116
84
58
anti-ALPHA
anti-BETA
C
D
1 2 3 4
1 2 3 4
180
116
84
58

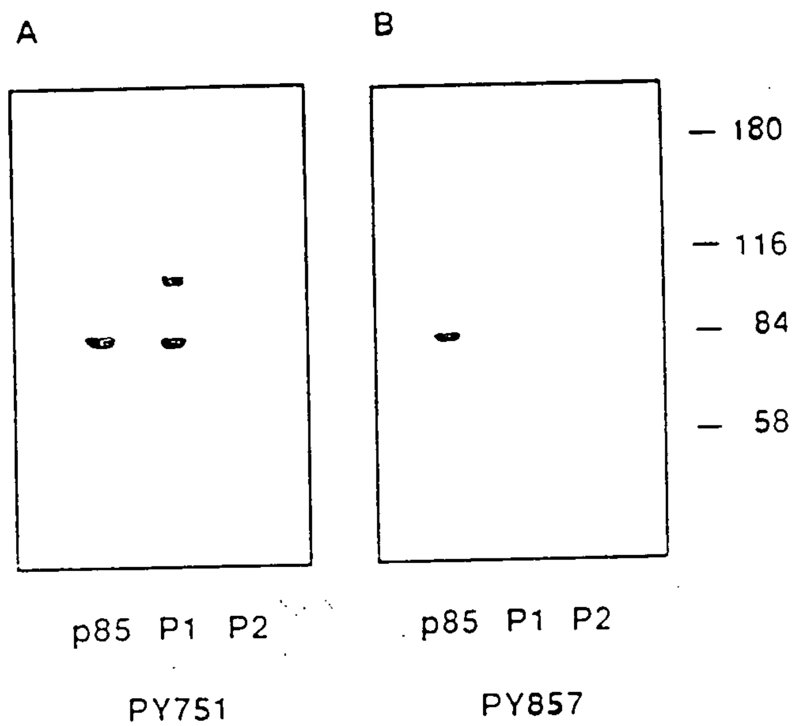


Figure 5

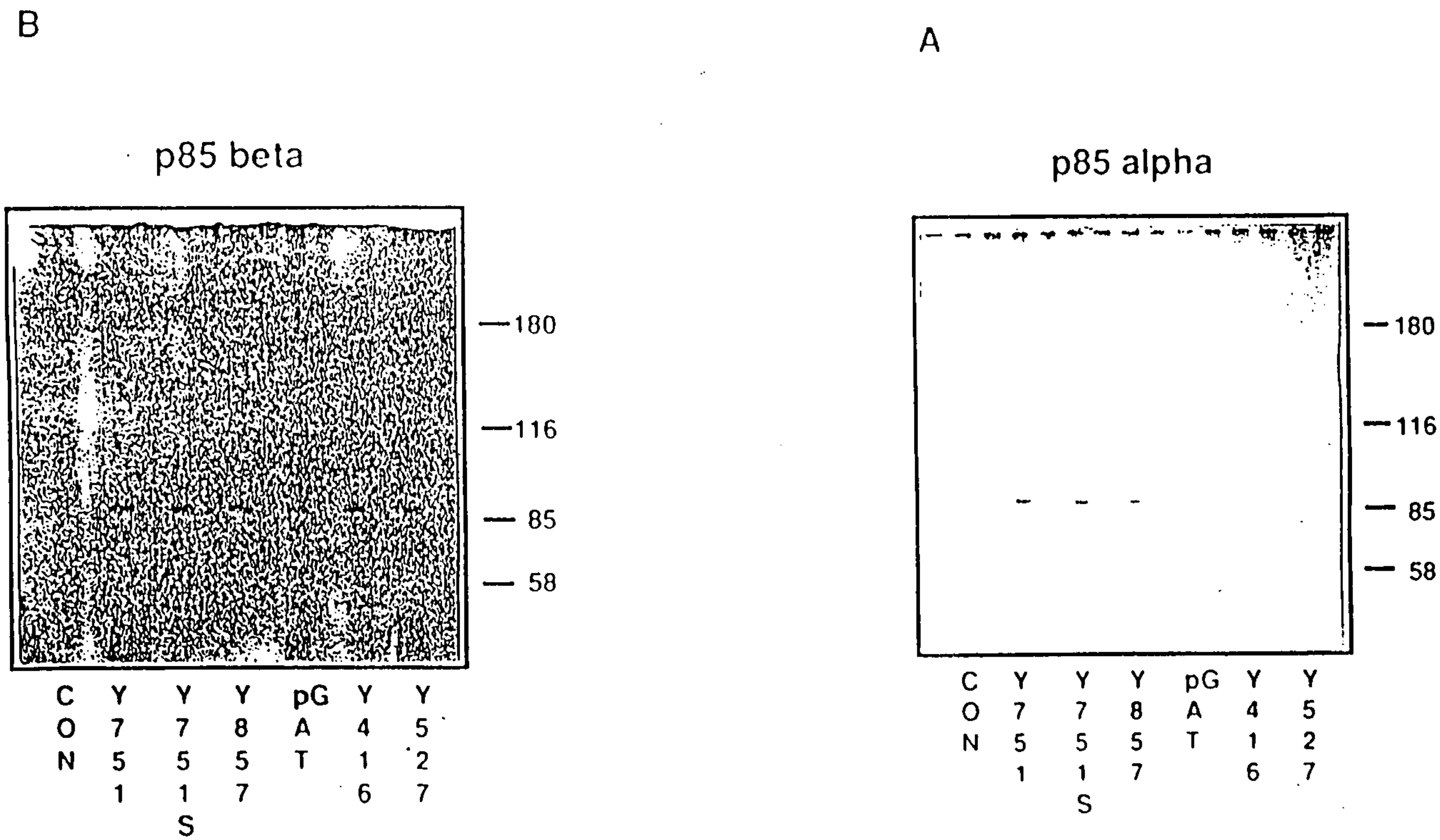
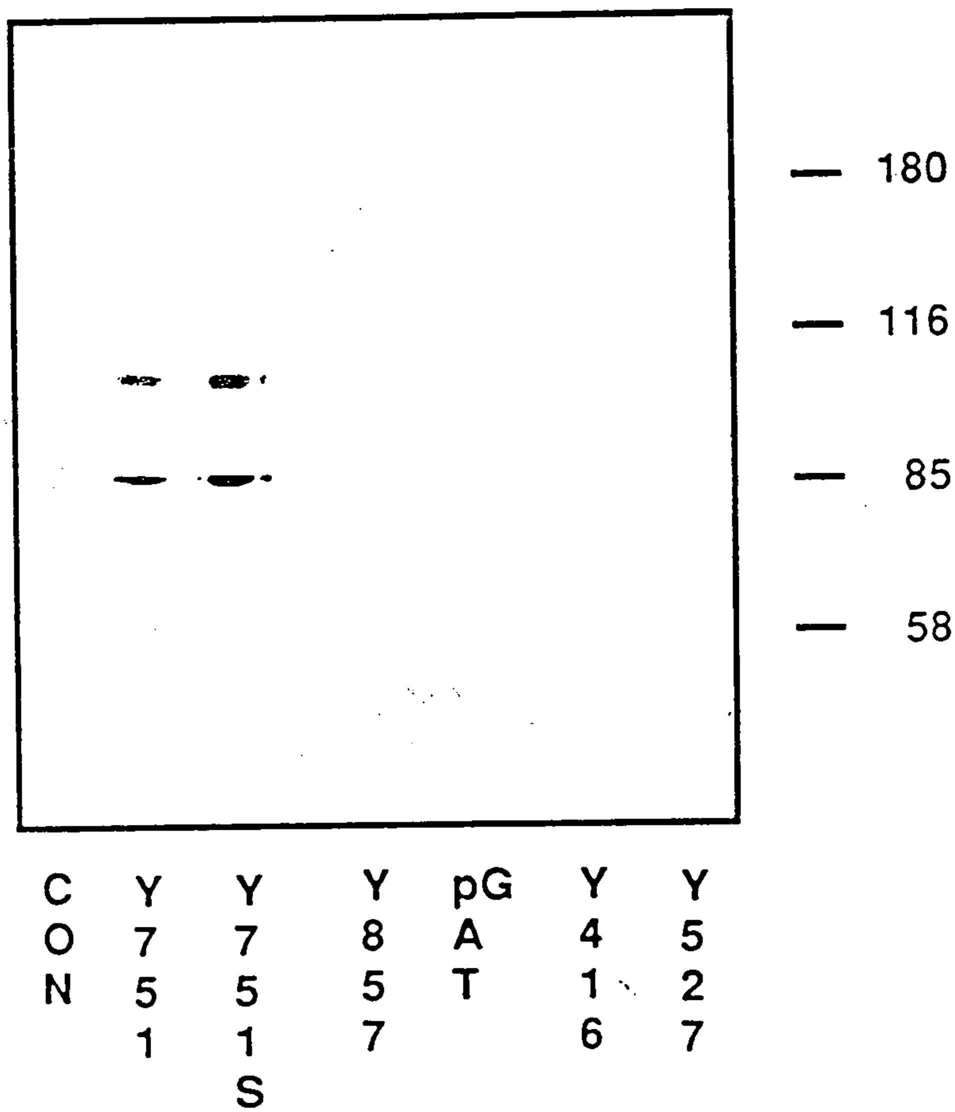

B
p85 beta
180
116
85
58
C O N
Y 7 5 1
Y 7 5 1 S
Y 8 5 7
pG A T
Y 4 1 6
Y 5 2 7
A
p85 alpha
180
116
85
58
C O N
Y 7 5 1
Y 7 5 1 S
Y 8 5 7
pG A T
Y 4 1 6
Y 5 2 7

Figure 6

Figure 7

A



B

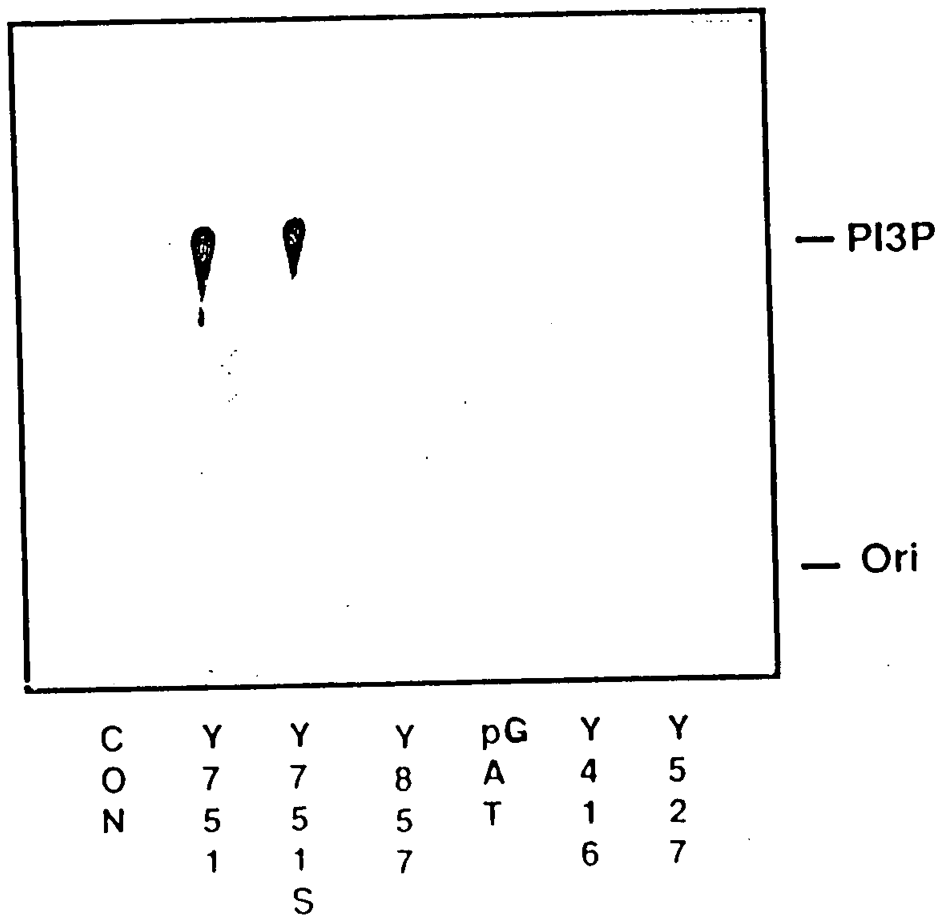
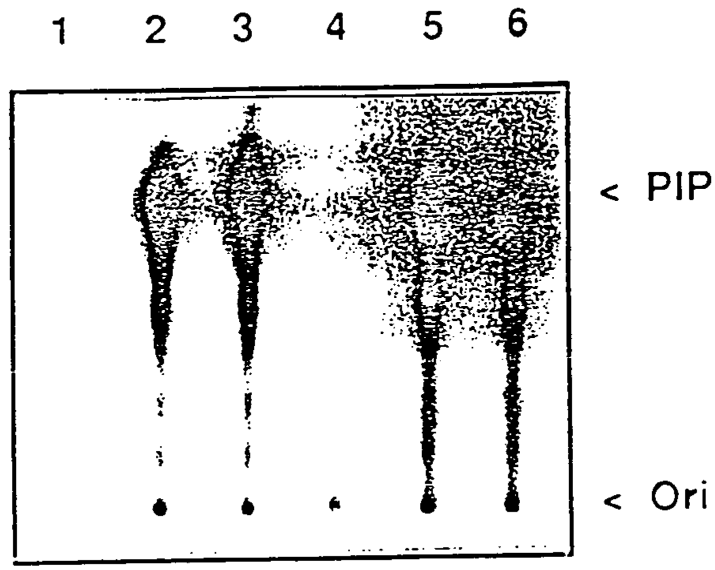


FIG 7 (contd)

Figure 8



751	D	M	S	K	D	E	S	V	D	Y	V	P	M	L	D	M	K
751.S				C	D	E	S	V	D	Y	V	P	M	L			
740				G	E	S	D	G	G	Y	M	D	M	S	K		
1313			E	F	C	P	D	P	L	Y	E	V	M	L	K		
Consensus					E	E	E	E	E	Y	M	P	M	X	X		
					D	D	D	D	D		V						

Figure 9

```
M  P  P  R  P  S  S  G  E  L  W  G  I  H  L  M       16
ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG     48

P  P  R  I  L  V  E  C  L  L  P  N  G  M  I  V       32
CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTG     96

T  L  E  C  L  R  E  A  T  L  I  T  I  K  H  E       48
ACTTTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA    144

L  F  K  E  A  R  K  Y  P  L  H  Q  L  L  Q  D       64
CTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGAT    192

E  S  S  Y  I  F  V  S  V  T  Q  E  A  E  R  E       80
GAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA    240

E  F  F  D  E  T  R  R  L  C  D  L  R  L  F  Q       96
GAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA    288

P  F  L  K  V  I  E  P  V  G  N  R  E  E  K  I      112
CCCTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC    336

L  N  R  E  I  G  F  A  I  G  M  P  V  C  E  F      128
CTCAATCGAGAAATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTC    384

D  M  V  K  D  P  E  V  Q  D  F  R  R  N  I  L      144
GATATGGTTAAAGATCCAGAAGTACAGGACTTCCGAAGAAATATTCTC    432
```

```
                N  V  C  K  E  A  V  D  L  R  D  L  N  S  P  H     160
FIG 9 (contd)   AATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT   480
                                     A
                S  R  A  M  Y  V  Y  P  P  N  V  E  S  S  P  E     176
                AGTAGAGCAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCAGAA   528

                L  P  K  H  I  Y  N  K  L  D  K  G  Q  I  I  V     192
                CTGCCAAAGCACATATATAATAAATTGGATAAAGGGCAAATAATAGTG   576

                V  I  W  V  I  V  S  P  N  N  D  K  Q  K  Y  T     208
                GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAACAGAAGTATACT   624

                L  K  I  N  H  D  C  V  P  E  Q  V  I  A  E  A     224
                CTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATTGCTGAAGCA   672

                I  R  K  K  T  R  S  M  L  L  S  S  E  Q  L  K     240
                ATCAGGAAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAAA   720

                L  C  V  L  E  Y  Q  G  K  Y  I  L  K  V  C  G     256
                CTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA   768

                C  D  E  Y  F  L  E  K  Y  P  L  S  Q  Y  K  Y     272
                TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT   816

                I  R  S  C  I  M  L  G  R  M  P  N  L  M  L  M     288
                ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGATGCTGATG   864
```

FIG 9 (contd)

```
A K E S L Y S Q L P M D C F T M                    304
GCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGACTGTTTTACAATG   912

P S Y S R R I S T A T P Y M N G                    320
CCATCATATTCCAGACGCATCTCCACAGCTACGCCATATATGAATGGA   960
                         B
E T S T K S L W V I N S A L R I                    336
GAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCACTCAGAATA   1008

K I L C A T Y V N V N I R D I D                    352
AAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGACATTGAC   1056

K I Y V R T G I Y H G G E P L C                    368
AAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTTATGT   1104

D N V N T Q R V P C S N P R W N                    384
GATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT   1152

E W L N Y D I Y I P D L P R A A                    400
GAATGGCTGAATTACGATATATACATTCCTGATCTTCCTCGTGCTGCT   1200

R L C L S I C S V K G R K G A K                    416
CGACTTTGCCTTTCCATTTGTTCTGTTAAAGGCCGAAAGGGTGCTAAA   1248

E E H C P L A W G N I N L F D Y                    432
GAGGAACACTGTCCATTGGCCTGGGGAAATATAAACTTGTTTGATTAC   1296
```

FIG. 9 (contd)

```
T  D  T  L  V  S  G  K  M  A  L  N  L  W  P  V     448
ACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTA   1344
                        C
P  H  G  L  E  D  L  L  N  P  I  G  V  T  G  S     464
CCTCATGGACTAGAAGATTTGCTGAACCCTATTGGTGTTACTGGATCA   1392

N  P  N  K  E  T  P  C  L  E  L  E  F  D  W  F     480
AATCCAAATAAAGAAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTC   1440

S  S  V  V  K  F  P  D  M  S  V  I  E  E  H  A     496
AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCC   1488

N  W  S  V  S  R  E  A  G  F  S  Y  S  H  A  G     512
AATTGGTCTGTATCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGA   1536

L  S  N  R  L  A  R  D  N  E  L  R  E  N  D  K     528
CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGAGAAAATGATAAA   1584

E  Q  L  R  A  I  C  T  R  D  P  L  S  E  I  T     544
GAACAGCTCCGAGCAATTTGTACACGAGATCCTCTATCTGAAATCACT   1632

E  Q  E  K  D  F  L  W  S  H  R  H  Y  C  V  T     560
GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAACT   1680

I  P  E  I  L  P  K  L  L  L  S  V  K  W  N  S     576
ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAACTCT   1728
```

FIG 9 (contd)

```
R  D  E  V  A  Q  M  Y  C  L  V  K  D  W  P  P      592
AGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGATTGGCCTCCA    1776

I  K  P  E  Q  A  M  E  L  L  D  C  N  Y  P  D      608
ATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGAT    1824

P  M  V  R  G  F  A  V  R  C  L  E  K  Y  L  T      624
CCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTAGAAAAATATTTAACA    1872
                              D
D  D  K  L  S  Q  Y  L  I  Q  L  V  Q  V  L  K      640
GATGACAAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAAA    1920

Y  E  Q  Y  L  D  N  L  L  V  R  F  L  L  K  K      656
TATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTTACTCAAAAAA    1968
                              E
A  L  T  N  Q  R  I  G  H  F  F  F  W  H  L  K      672
GCGTTAACTAATCAAAGGATCGGTCACTTTTTCTTTTGGCATTTAAAA    2016
                                           F
S  E  M  H  N  K  T  V  S  Q  R  F  G  L  L  L      688
TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTTG    2064

E  S  Y  C  R  A  C  G  M  Y  L  K  H  L  N  R      704
GAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGG    2112
                                        G
Q  V  E  A  M  E  K  L  I  N  L  T  D  I  L  K      720
CAAGTTGAGGCTATGGAAAAGCTCATTAACTTGACTGACATTCTCAAA    2160
```

FIG 9 (contd)

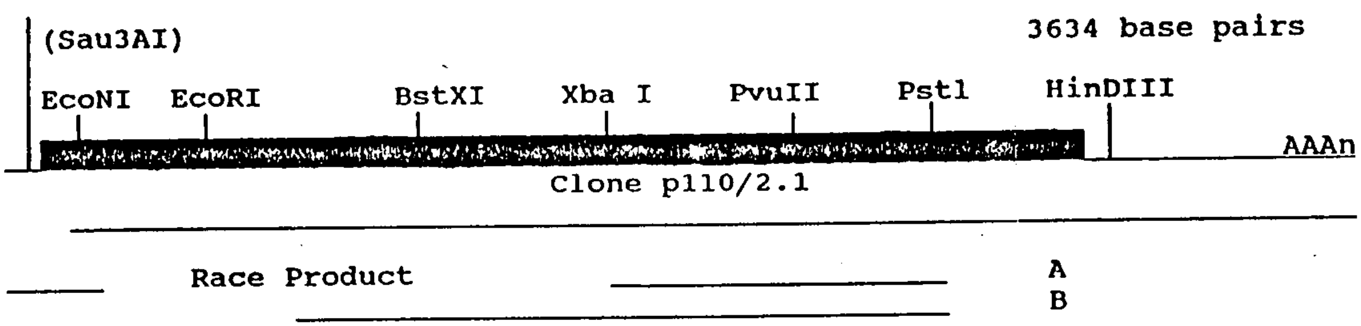
```
Q  E  K  K  D  E  T  Q  K  V  Q  M  K  F  L  V      736
CAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT   2208

E  Q  M  R  R  P  D  F  M  D  A  L  Q  G  F  L      752
GAGCAAATGCGGCGACCAGATTTCATGGATGCTCTCCAGGGCTTTCTG   2256

S  P  L  N  P  A  H  Q  L  G  N  L  R  L  E  E      768
TCTCCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAG   2304

C  R  I  M  S  S  A  K  R  P  L  W  L  N  W  E      784
TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG   2352

N  P  D  I  M  S  E  L  L  F  Q  N  N  E  I  I      800
AACCCAGACATCATGTCAGAATTACTCTTTCAGAACAATGAGATCATC   2400

F  K  N  G  D  D  L  R  Q  D  M  L  T  L  Q  I      816
TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATT   2448

I  R  I  M  E  N  I  W  Q  N  Q  G  L  D  L  R      832
ATTCGCATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGA   2496

M  L  P  Y  G  C  L  S  I  G  D  C  V  G  L  I      848
ATGTTACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC   2544

E  V  V  R  N  S  H  T  I  M  Q  I  Q  C  K  G      864
GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAAGGA   2592
```

FIG 9 (contd)

```
                                   H
 G  L  K  G  A  L  Q  F  N  S  H  T  L  H  Q  W       880
GGCCTGAAAGGTGCACTGCAGTTTAACAGCCACACACTCCATCAGTGG     2640

 L  K  D  K  N  K  G  E  I  Y  D  A  A  I  D  L       896
CTCAAAGACAAGAACAAGGGGGAAATATATGATGCGGCCATCGATTTG     2688
               I
 F  T  R  S  C  A  G  Y  C  V  A  T  F  I  L  G       912
TTTACACGATCATGTGCTGGATATTGTGTTGCCACCTTCATTTTGGGA     2736

 I  G  D  R  H  N  S  N  I  M  V  K  D  D  G  Q       928
ATTGGAGATCGTCACAATAGTAATATCATGGTTAAAGATGATGGACAA     2784
                  J
 L  F  H  I  D  F  G  H  F  L  D  H  K  K  K  K       944
CTGTTTCATATAGATTTTGGACACTTTTTGGATCACAAGAAGAAAAAA     2832
                                K
 F  G  Y  K  R  E  R  V  P  F  V  L  T  Q  D  F       960
TTTGGTTATAAACGAGAGCGCGTGCCGTTTGTTTTGACACAAGATTTC     2880

 L  I  V  I  S  K  G  A  Q  E  C  T  K  T  R  E       976
TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA     2928

 F  E  R  F  Q  E  M  C  Y  K  A  Y  L  A  I  R       992
TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGG     2976
```

FIG 9 (contd)

```
                                L
Q   H   A   N   L   F   I   N   L   F   S   M   M   L   G   S     1008
CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT                  3024

G   M   P   E   L   Q   S   F   D   D   I   A   Y   I   R   K     1024
GGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATTCGAAAG                  3072
                                              M
T   L   A   L   D   K   T   E   Q   E   A   L   E   Y   F   M     1040
ACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG                  3120

K   Q   M   N   D   A   H   H   G   G   W   T   T   K   M   D     1056
AAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAAATGGAT                  3168
            N
W   I   F   H   T   I   K   Q   H   A   L   N   *     1069
TGGATCTTCCACACAATTAAGCAGCATGCTTTGAACTGA               3207
```



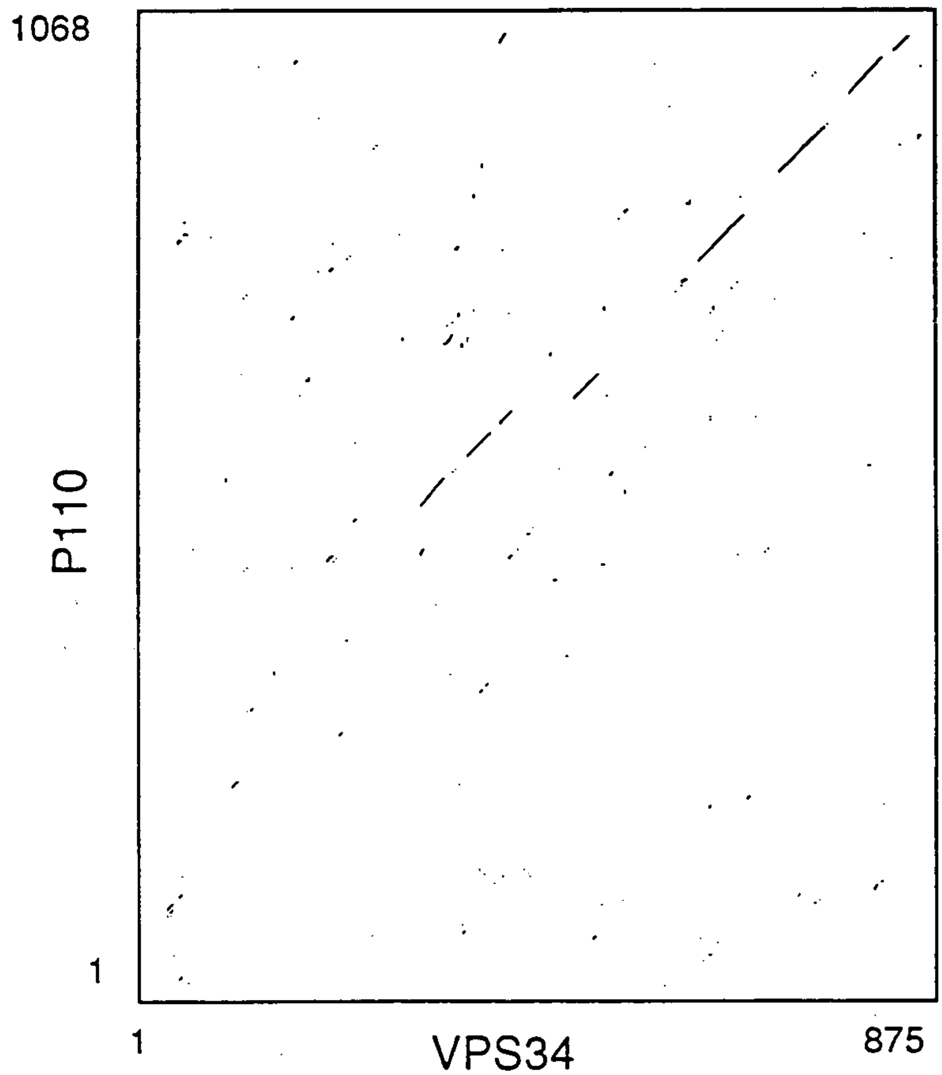


Figure 10 A

Figure 10 B

```
P110        VCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPN 170
              ..| : .| :|. :: .| .:  . . |:. ..  ...: :...|
VPS34       NITFCVSQDLDVP.LKVKIKSLEGHKPLLKPSQKILNPELMLIGSN 49

       171 VESSPEL..PKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE 218
           | .|.:|  . ::::|  . .:.:.|:.   | .:.......:
        50 VFPSSDLIVSLQVFDKERNRNLTLPIYTPYIPFRNSRTWDYWL....... 92

       219 QVIAEAIRKKTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLS 268
                .:. :.: : :|| :|::.::||.|
        93 .....TLPIRIKQLTFSS.HLRIILWEYNG..................... 116

       269 QYKYIRSCIMLGRMPNLMIMAKESLYSQLPMDCFTMPSYSRRISTATPYM 318
                                                       |...|::
       117 ...........................................SKQIPFF 123

       319 NGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC 368
           | |||.  : : ::.|:              |:::.: .| ::.. .|.:.
       124 NLETSI..FNLKDCTLK..............RGFESLKFRYDVIDHCEVVT 158

       369 DNVNTQRVPCSNPRWNEWLNYDIYIPDLPRAARLC.LSICSVKGRKGAKE 417
           || :         .| || ..: .::.| ::|  :.|:.:: .::.:.
       159 DNKD...........QENLN.KYFQGEFTRLPWLDEITISKLRKQRENRT 196
```

Fig 10 B (contd)

```
                .         .         .         .         .
418 .EHCPLAWG.NINLFDYTDTLVSGKMALNLWPVPHGLEDLLNPIGVTGS. 464
     .:..:.:. :: ::::.. .::. .:  .    :|     .| |  |:...
197 WPQGTFVLNLEFPMLELPVVFIERE IMNTQMNIP....TLKNNPGLSTDL 242

                .         .         .         .         .
465 .NPNKETPCLELEF.DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAG 512
     :||::.| :.:.: |.: |.:|| |     .:::| ..  |   ...:|:
243 REPNRNDPQIKISLGDKYHSTLKFYD....PDQPNNDPIEEKYRRLERAS 288

                .         .         .         .         .
513 LSNRLARDNELRENDKEQLRAICTRDPLSEITEQEKDFLWSHRHYCVTIP 562
     ...|.:: .   ..:: |. |.. .| ..:|.:||: :|..|.| :. .
289 KNANLDKQVKPDIKKRDYLNKIINYPPGTKLTAHEKGSIWKYRYYILMNNK 338

                .         .         .         .         .
563 EILPKLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAMELLDCNYPDPMVR 612
    . |.||| |..:.. .| .::. |:..|:.|. ::|:|||::.:.:  ||
339 KALTKLLQSTNLREESERVEVLELMDSWAEIDIDDALELLGSTFKNLSVR 388

                .         .         .         .         .
613 GFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQY.................. 644
    ::||. |.|  .|..|. ||:|||:.: :|..
389 SYAVNRLKK.ASDKELELYLLQLVEAVCFENLSTFSDKSNSEFTIVDAVS 437

                .         .         .         .         .
645 ...................................LDNLLVRFLLKK 656
                                       : . |. ||:::
438 SQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLPIVISPLAEFLIRR 487
```

Fig. 10 B (contd)

```
                    .         .         .         .         .
657 ALTNQRIGHFFFWHLKSEMHNKTVSQRFGLLLESY.CRACGMYLKHLNRQ 705
    ||.|.|:| ||:|.|||| .:|.    :: :|.|: :|    .  . || |
488 ALVNPRLGSFFYWYLKSESEDKPY...LDQILSSFWSRLDKKSRNILNDQ 534

                    .         .         .         .         .
706 VEAMEKLINLTDILKQEKKDETQKVQMKF.LVEQMRRPDFMDALQGFLSP 754
    |  :: | : .:.:|. |.....|::: . |:| . ||  :  :..:  |
535 VRLINVLRECCETIKRLKDTTAKKMELLVHLLETKVRP..LVKVRPIALP 582

                    .         .         .         .         .
755 LNPAHQLGNLRLEECRIMSSAKRPLWLNWENPDIMSELLFQNNEIIFKNG 804
    |:|.  :.:: |.::::.|. .||.:.:...      | |  .::|| |
583 LDPDVLICDVCPETSKVFKSSLSPLKITFKTT......LNQPYHLMFKVG 626

                    .         .         .        *.         .
805 DDLRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNS 854
    |||||| |.:|||.:|::::.|:.:||:: || .|..|.  | ||.:.|
627 DDLRQDQLVVQIISLMNELLKNENVDLKLTPYKILATGPQEGAIEFIPN. 675

             *.         .         .         .         .
855 HTIMQIQCK.GGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRSCAG 903
    .|: | :| |: | |.:          :: .:... :: : .:| |.:||||
676 DTLASILSKYHGILGYLKL......HYPDENATLGVQGWVLDNFVKSCAG 719

                    . *    *  .         ***       .         .
904 YCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVP 953
    ||| |:|||:|||| .|::|..||::|| |||.:|::..|.|       |
720 YCVITYILGVGDRHLDNLLVTPDGHFFHADFGYILGQDPKPF.......P 762
```

Fig 10 B (contd)

```
              .         .         .         .         .
 954 FVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLFS 1003
      ::. .  |: .|:.|:.   ::::|.. |: ||  :|.:|.|::|||.
 763 PLMKLPPQIIEAFGGAESS...NYDKFRSYCFVAYSILRRNAGLILNLFE 809

              .         .         .         .         .
1004 MMLGSGMPE..LQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGW 1051
     :| .|.:|:  ::. :.|  :|. :.|:..|::|  .| . :||. :: :
 810 LMKTSNIPDIRIDPNGAILRVRERFNLNMSEEDATVHFQNLINDSVNALL 859

              .
1052 TTKMDWIFHTIKQH 1065
     .. :|  :|.: |.
 860 PIVIDH.LHNLAQY 872
```

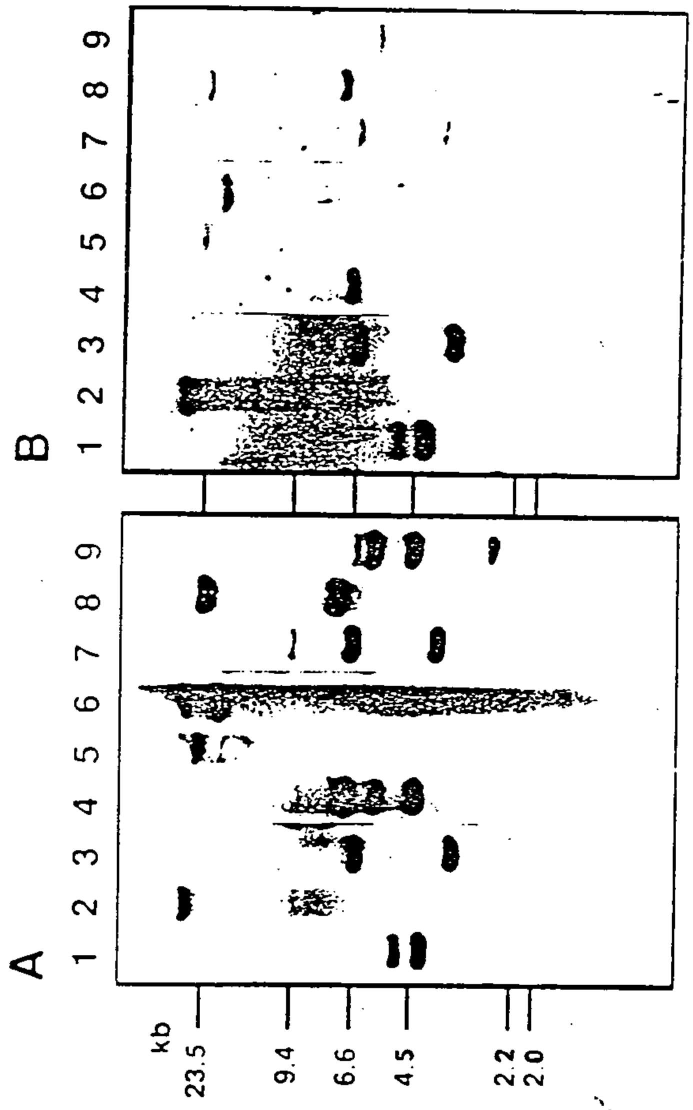


Figure 11

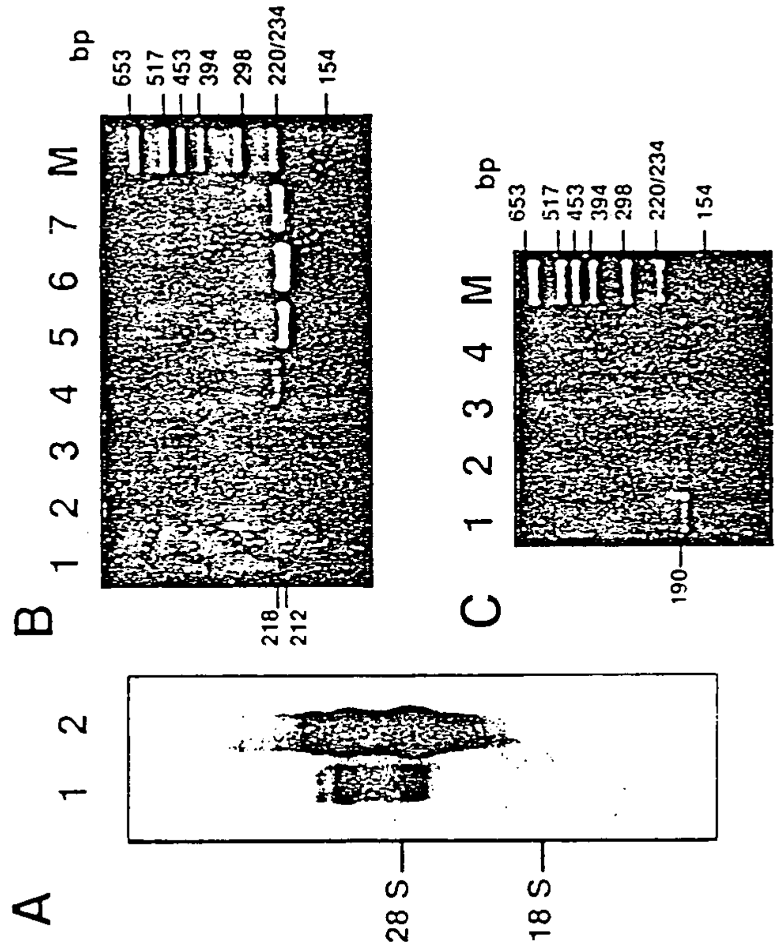

A
1
2
28 S
18 S
B
1
2
3
4
5
6
7
M
bp
653
517
453
394
298
220/234
154
218
212
C
1
2
3
4
M
bp
653
517
453
394
298
220/234
154
190

Figure 12

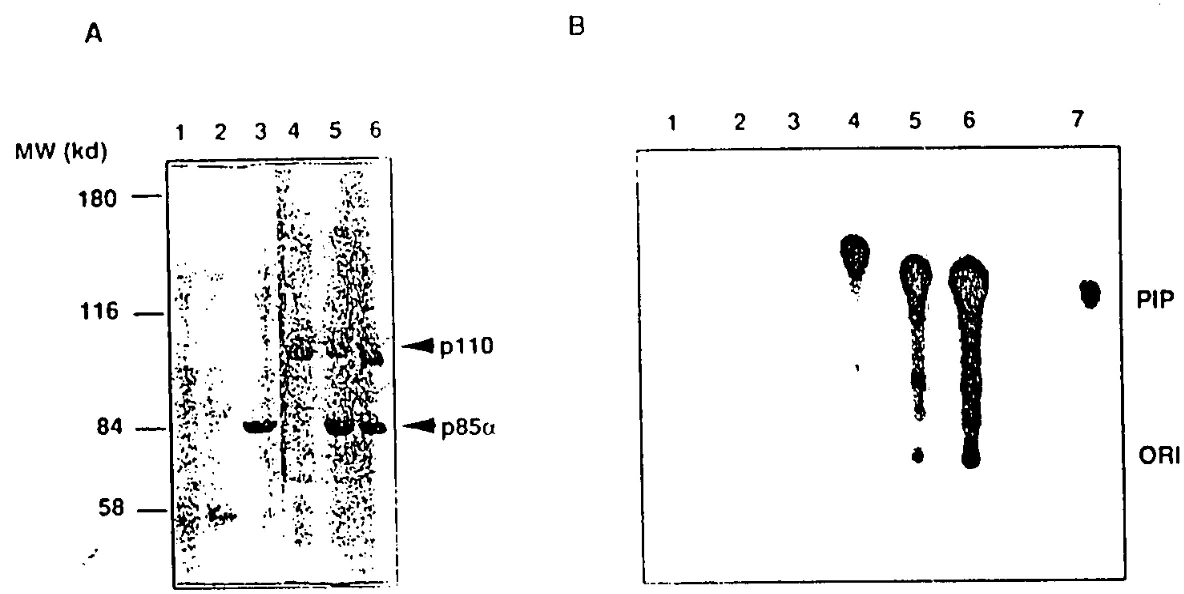


Figure 13

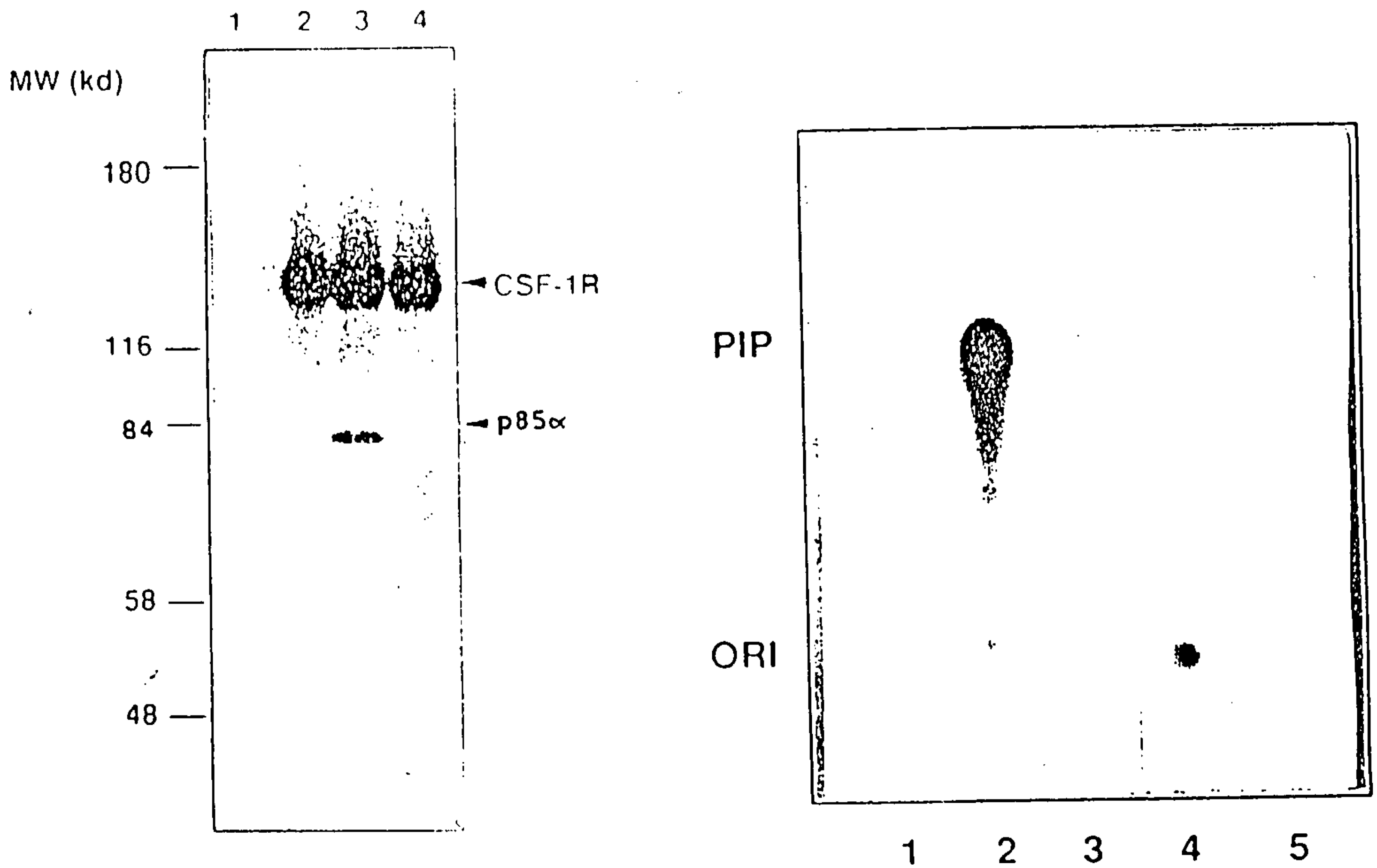
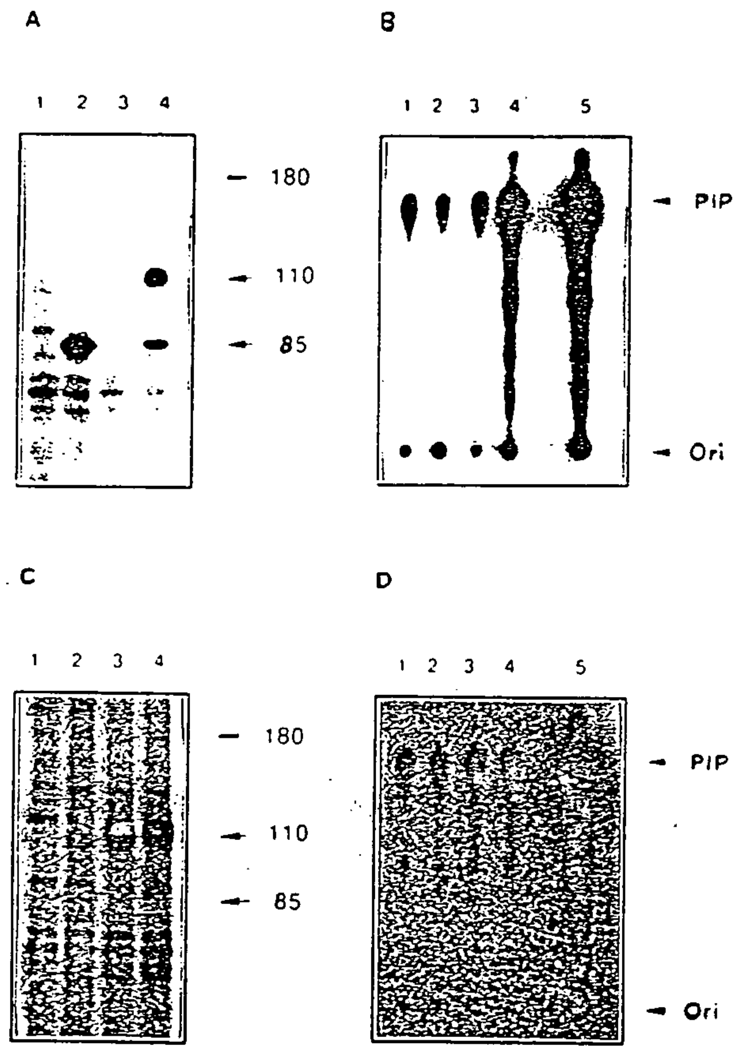


Figure 14

Figure 15


A
1 2 3 4
180
110
85
B
1 2 3 4 5
PIP
Ori
C
1 2 3 4
180
110
85
D
1 2 3 4 5
PIP
Ori

The human p110 cDNA nucleotide and deduced amino acid sequence.

```
     ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG
  1  ---------+---------+---------+---------+--------  48
     TACGGAGGTTCTGGTAGTAGTCCACTTGACACCCCGTAGGTGAACTAC
     M  P  P  R  P  S  S  G  E  L  W  G  I  H  L  M

     CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTG
 49  -+---------+---------+---------+---------+------  96
     GGGGGTTCTTAGGATCACCTTACAAATGATGGTTTACCTTACTATCAC
     P  P  R  I  L  V  E  C  L  L  P  N  G  M  I  V

     ACTTTAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAAGCATGAA
 97  ---+---------+---------+---------+---------+----  144
     TGAAATCTTACGGAGGCACTCCGATGTAATCATTGATATTTCGTACTT
     T  L  E  C  L  R  E  A  T  L  V  T  I  K  H  E

     CTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGAT
145  -----+---------+---------+---------+---------+--  192
     GATAAATTTCTTCGTTCTTTTATGGGAGAGGTAGTTGAAGAAGTTCTA
     L  F  K  E  A  R  K  Y  P  L  H  Q  L  L  Q  D
```

Figure 16

```
     GAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA
193  --------+---------+---------+---------+---------+  240
     CTTAGAAGAATGTAAAAGCATTCACAATGGGTTCTTCGTCTTTCCCTT
     E  S  S  Y  I  F  V  S  V  T  Q  E  A  E  R  E

     GAATTTTTTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA
241  ----------+---------+---------+---------+--------  288
     CTTAAAAAACTACTTTGTTCTGCTGAAACACTAGAAGCCGAAAAAGTT
     E  F  F  D  E  T  R  R  L  C  D  L  R  L  F  Q

     CCATTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC
289  -+---------+---------+---------+---------+------  336
     GGTAAAAATTTTCATTAACTTGGTCATCCGTTGGCACTTCTTTTCTAG
     P  F  L  K  V  I  E  P  V  G  N  R  E  E  K  I

     CTCAATCGAGAAATTGGTTTTGCTATCGGCATGCCAGTGTGCGAATTT
337  ---+---------+---------+---------+---------+----  384
     GAGTTAGCTCTTTAACCAAAACGATAGCCGTACGGTCACACGCTTAAA
     L  N  R  E  I  G  F  A  I  G  M  P  V  C  E  F
```

FIG 16 (contd)

```
     GATATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGAAATATTCTT
385  -----+---------+---------+---------+---------+--  432
     CTATACCAATTTCTAGGACTTCATGTCCTGAAGGCTTCTTTATAAGAA
     D  M  V  K  D  P  E  V  Q  D  F  R  R  N  I  L

     AATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT
433  -------+---------+---------+---------+---------+  480
     TTACAAACATTTCTTCGACACCTAGAATCCCTAGAATTAAGTGGAGTA
     N  V  C  K  E  A  V  D  L  R  D  L  N  S  P  H

     AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG
481  ---------+---------+---------+---------+--------  528
     TCATCTCGTTACATACAGATAGGCGGTGTACATCTTAGAAGTGGTCTC
     S  R  A  M  Y  V  Y  P  P  H  V  E  S  S  P  E

     CTGCCAAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTG
529  -+---------+---------+---------+---------+------  576
     GACGGTTTCGTGTATATATTATTTAACCTATCTCCGGTTTATTATCAC
     L  P  K  H  I  Y  N  K  L  D  R  G  Q  I  I  V
```

FIG 16 (contd)

```
      GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAGCAGAAGTATACT
577   ---+---------+---------+---------+---------+----   624
      CACTAAACCCATTATCAAAGAGGTTTATTACTGTTCGTCTTCATATGA
      V  I  W  V  I  V  S  P  N  N  D  K  Q  K  Y  T

      CTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATTGCTGAAGCA
625   -----+---------+---------+---------+---------+--   672
      GACTTTTAGTTGGTACTGACACACGGTCTTGTTCATTAACGACTTCGT
      L  K  I  N  H  D  C  V  P  E  Q  V  I  A  E  A

      ATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCTGAACAATTAAAA
673   -------+---------+---------+---------+---------+   720
      TAGTCCTTTTTTTGATCTTCATACAACGATAGTAGACTTGTTAATTTT
      I  R  K  K  T  R  S  M  L  L  S  S  E  Q  L  K

      CTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGA
721   ---------+---------+---------+---------+--------   768
      GAGACACAAAATCTTATAGTCCCGTTCATGTAAAATTTTCACACACCT
      L  C  V  L  E  Y  Q  G  K  Y  I  L  K  V  C  G
```

FIG 16 (contd)

```
     TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT
769  -+---------+---------+---------+---------+------  816
     ACACTACTTATGAAGGATCTTTTTATAGGAGACTCAGTCATATTCATA
     C  D  E  Y  F  L  E  K  Y  P  L  S  Q  Y  K  Y

     ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGAAGATGATG
817  ---+---------+---------+---------+---------+----  864
     TATTCTTCGACATATTACGAACCCTCCTACGGGTTAAACTTCTACTAC
     I  R  S  C  I  M  L  G  R  M  P  N  L  K  M  M

     GCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGACTGTTTTACAATG
865  -----+---------+---------+---------+---------+--  912
     CGATTTCTTTCGGAAATAAGAGTTGACGGTTACCTGACAAAATGTTAC
     A  K  E  S  L  Y  S  Q  L  P  M  D  C  F  T  M

     CCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA
913  -------+---------+---------+---------+---------+  960
     GGTAGAATAAGGTCTGCGTAAAGGTGTCGATGTGGTATATACTTACCT
     P  S  Y  S  R  R  I  S  T  A  T  P  Y  M  N  G
```

FIG 16 (contd)

```
     GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA
 961 ---------+---------+---------+---------+-------- 1008
     CTTTGTAGATGTTTTAGGGAAACCCAATATTTATCTCGTGAGTCTTAT
     E  T  S  T  K  S  L  W  V  I  N  R  A  L  R  I

     AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC
1009 -+---------+---------+---------+---------+------ 1056
     TTTTAAGAAACACGTTGGATGCACTTAGATTTATAAGCTCTGTAACTG
     K  I  L  C  A  T  Y  V  N  L  N  I  R  D  I  D

     AAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTTATGT
1057 ---+---------+---------+---------+---------+---- 1104
     TTCTAAATACAAGCTTGTCCATAGATGGTACCTCCTCTTGGGAATACA
     K  I  Y  V  R  T  G  I  Y  H  G  G  E  P  L  C

     GACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT
1105 -----+---------+---------+---------+---------+-- 1152
     CTGTTACACTTGTGAGTTTCTCATGGAACAAGGTTAGGGTCCACCTTA
     D  N  V  N  T  Q  R  V  P  C  S  N  P  R  W  N
```

FIG 16 (contd)

```
       GAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT
1153   -------+---------+---------+---------+---------+   1200
       CTTACCGACTTAATACTATATATGTAAGGACTAGAAGGAGCACGACGA
       E  W  L  N  Y  D  I  Y  I  P  D  L  P  R  A  A

       CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAA
1201   ---------+---------+---------+---------+--------   1248
       GCTGAAACGGAAAGGTAAACGAGACAATTTCCGGCTTTCCCACGATTT
       R  L  C  L  S  I  C  S  V  K  G  R  K  G  A  K

       GAGGAACACTGTCCATTGGCATGGGGAAATATAAACTTGTTTGATTAC
1249   -+---------+---------+---------+---------+------   1296
       CTCCTTGTGACAGGTAACCGTACCCCTTTATATTTGAACAAACTAATG
       E  E  H  C  P  L  A  W  G  N  I  N  L  F  D  Y

       ACAGACACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTA
1297   ---+---------+---------+---------+---------+----   1344
       TGTCTGTGAGATCATAGACCTTTTTACCGAAACTTAGAAACCGGTCAT
       T  D  T  L  V  S  G  K  M  A  L  N  L  W  P  V
```

FIG 16 (contd)

```
       CCTCATGGATTAGAAGATTTGCTGAACCCTATTGGTGTTACTGGATCA
1345   -----+---------+---------+---------+---------+--   1392
       GGAGTACCTAATCTTCTAAACGACTTGGGATAACCACAATGACCTAGT
       P  H  G  L  E  D  L  L  N  P  I  G  V  T  G  S

       AATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC
1393   -------+---------+---------+---------+---------+   1440
       TTAGGTTTATTTCTTTGAGGTACGAATCTCAACCTCAAACTGACCAAG
       N  P  N  K  E  T  P  C  L  E  L  E  F  D  W  F

       AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC
1441   ---------+---------+---------+---------+--------   1488
       TCGTCACACCATTTCAAGGGTCTATACAGTCACTAACTTCTCGTACGG
       S  S  V  V  K  F  P  D  M  S  V  I  E  E  H  A

       AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGA
1489   -+---------+---------+---------+---------+------   1536
       TTAACCAGACATAGGGCTCTTCGTCCTAAATCGATAAGGGTGCGTCCT
       N  W  S  V  S  R  E  A  G  F  S  Y  S  H  A  G
```

FIG 16 (contd)

```
      CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAA
1537  ---+---------+---------+---------+---------+----  1584
      GACTCATTGTCTGATCGATCTCTGTTACTTAATTCCCTTTTACTGTTT
      L  S  N  R  L  A  R  D  N  E  L  R  E  N  D  K

      GAACAGCTCAAAGCAATTTCTACACGAGATCCTCTCTCTGAAATCACT
1585  -----+---------+---------+---------+---------+--  1632
      CTTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGAGACTTTAGTGA
      E  Q  L  K  A  I  S  T  R  D  P  L  S  E  I  T

      GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAACT
1633  -------+---------+---------+---------+---------+  1680
      CTCGTCCTCTTTCTAAAAGATACCTCAGTGTCTGTGATAACACATTGA
      E  Q  E  K  D  F  L  W  S  H  R  H  Y  C  V  T

      ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAATTCT
1681  ---------+---------+---------+---------+--------  1728
      TAGGGGCTTTAAGATGGGTTTAACGAAGACAGACAATTTACCTTAAGA
      I  P  E  I  L  P  K  L  L  L  S  V  K  W  N  S
```

FIG 16 (contd)

```
        AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCA
1729    -+---------+---------+---------+---------+------    1776
        TCTCTACTTCATCGGGTCTACATAACGAACCATTTTCTAACCGGAGGT
        R  D  E  V  A  Q  M  Y  C  L  V  K  D  W  P  P

        ATCAAACCTGAACAGGCTATGGAACTTCTGGACTGTAATTACCCAGAT
1777    ---+---------+---------+---------+---------+----    1824
        TAGTTTGGACTTGTCCGATACCTTGAAGACCTGACATTAATGGGTCTA
        I  K  P  E  Q  A  M  E  L  L  D  C  N  Y  P  D

        CCTATGGTTCGAGGTTTTGCTGTTCGGTGCTTGGAAAAATATTTAACA
1825    -----+---------+---------+---------+---------+--    1872
        GGATACCAAGCTCCAAAACGACAAGCCACGAACCTTTTTATAAATTGT
        P  M  V  R  G  F  A  V  R  C  L  E  K  Y  L  T

        GATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA
1873    -------+---------+---------+---------+---------+    1920
        CTACTGTTTGAAAGAGTCATAAATTAAGTCGATCATGTCCAGGATTTT
        D  D  K  L  S  Q  Y  L  I  Q  L  V  Q  V  L  K
```

FIG 16 (contd)

```
       TATGAACAATATTTGGATAACTTGCTTGTGAGATTTTTACTGAAGAAA
1921   ---------+---------+---------+---------+--------   1968
       ATACTTGTTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT
       Y  E  Q  Y  L  D  N  L  L  V  R  F  L  L  K  K

       GCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTGGCATTTAAAA
1969   -+---------+---------+---------+---------+------   2016
       CGTAACTGATTAGTTTCCTAACCCGTGAAAAAGAAAACCGTAAATTTT
       A  L  T  N  Q  R  I  G  H  F  F  F  W  H  L  K

       TCTGAGATGCACAATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTG
2017   ---+---------+---------+---------+---------+----   2064
       AGACTCTACGTGTTATTTTGTCAATCGGTCTCCAAACCGGACGAAAAC
       S  E  M  H  N  K  T  V  S  Q  R  F  G  L  L  L

       GAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAGCACCTGAATAGG
2065   -----+---------+---------+---------+---------+--   2112
       CTCAGGATAACAGCACGTACACCCTACATAAACTTCGTGGACTTATCC
       E  S  Y  C  R  A  C  G  M  Y  L  K  H  L  N  R
```

FIG 16 (contd)

```
     CAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGACATTCTCAAA
2113 -------+---------+---------+---------+---------+ 2160
     GTTCAGCTCCGTTACCTTTTCGAGTAATTGAATTGACTGTAAGAGTTT
     Q  V  E  A  M  E  K  L  I  N  L  T  D  I  L  K

     CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT
2161 ---------+---------+---------+---------+-------- 2208
     GTCCTCTCCTTCCTACTTTGTGTTTTCCATGTCTACTTCAAAAATCAA
     Q  E  R  K  D  E  T  Q  K  V  Q  M  K  F  L  V

     GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTG
2209 -+---------+---------+---------+---------+------ 2256
     CTCGTTTACTCCGCTGGTCTAAAGTACCTACGGGATGTCCCGAACGAC
     E  Q  M  R  R  P  D  F  M  D  A  L  Q  G  L  L

     TCTCCTCTAAACCCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAG
2257 ---+---------+---------+---------+---------+---- 2304
     AGAGGAGATTTGGGACGAGTAGTTGATCCTTTGGAGTCCGAATTTCTC
     S  P  L  N  P  A  H  Q  L  G  N  L  R  L  K  E
```

FIG 16 (contd)

```
        TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG
2305    -----+---------+---------+---------+---------+--    2352
        ACAGCTTAATACAGAAGACGTTTTTCCGGTGACACCAACTTAACCCTC
        C  R  I  M  S  S  A  K  R  P  L  W  L  N  W  E

        AACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC
2353    -------+---------+---------+---------+---------+    2400
        TTGGGTCTGTAGTACAGTCTCAATGACAAAGTCTTGTTACTCTAGTAG
        N  P  D  I  M  S  E  L  L  F  Q  N  N  E  I  I

        TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT
2401    ---------+---------+---------+---------+--------    2448
        AAATTTTTACCCCTACTAAATGCCGTTCTATACGATTGTGAAGTTTAA
        F  K  N  G  D  D  L  R  Q  D  M  L  T  L  Q  I

        ATTCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGA
2449    -+---------+---------+---------+---------+------    2496
        TAAGCATAATACCTTTTATAGACCGTTTTAGTTCCAGAACTAGAAGCT
        I  R  I  M  E  N  I  W  Q  N  Q  G  L  D  L  R
```

FIG 16 (contd)

```
     ATGTTACCTTATGGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATT
2497 ---+---------+---------+---------+---------+---- 2544
     TACAATGGAATACCAACAGACAGTTAGCCACTGACACACCCTGAATAA
     M  L  P  Y  G  C  L  S  I  G  D  C  V  G  L  I

     GAGGTGGTGCGAAATTCTCACACTATTATGCAAATTCAGTGCAAAGGC
2545 -----+---------+---------+---------+---------+-- 2592
     CTCCACCACGCTTTAAGAGTGTGATAATACGTTTAAGTCACGTTTCCG
     E  V  V  R  N  S  H  T  I  M  Q  I  Q  C  K  G

     GGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG
2593 -------+---------+---------+---------+---------+ 2640
     CCGAACTTTCCACGTGACGTCAAGTTGTCGGTGTGTGATGTAGTCACC
     G  L  K  G  A  L  Q  F  N  S  H  T  L  H  Q  W

     CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG
2641 ---------+---------+---------+---------+-------- 2688
     GAGTTTCTGTTCTTGTTTCCTCTTTATATACTACGTCGGTAACTGGAC
     L  K  D  K  N  K  G  E  I  Y  D  A  A  I  D  L
```

FIG 16 (contd)

```
     TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGA
2689 -+---------+---------+---------+---------+------ 2736
     AAATGTGCAAGTACACGACCTATGACACATCGATGGAAGTAAAACCCT
     F  T  R  S  C  A  G  Y  C  V  A  T  F  I  L  G

     ATTGGAGATCGTCACAATAGTAACATCATGGTGAAAGACGATGGACAA
2737 ---+---------+---------+---------+---------+---- 2784
     TAACCTCTAGCAGTGTTATCATTGTAGTACCACTTTCTGCTACCTGTT
     I  G  D  R  H  N  S  N  I  M  V  K  D  D  G  Q

     CTGTTTCATATAGATTTTGGACACTTTTTGGATCACAAGAAGAAAAAA
2785 -----+---------+---------+---------+---------+-- 2832
     GACAAAGTATATCTAAAACCTGTGAAAAACCTAGTGTTCTTCTTTTTT
     L  F  H  I  D  F  G  H  F  L  D  H  K  K  K  K

     TTTGGTTATAAACGAGAACGTGTGCCATTTGTTTTGACACAGGATTTC
2833 -------+---------+---------+---------+---------+ 2880
     AAACCAATATTTGCTCTTGCACACGGTAAACAAAACTGTGTCCTAAAG
     F  G  Y  K  R  E  R  V  P  F  V  L  T  Q  D  F
```

FIG 16 (contd)

```
     TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA
2881 ---------+---------+---------+---------+-------- 2928
     AATTATCACTAATCATTTCCTCGGGTTCTTACGTGTTTCTGTTCTCTT
     L  I  V  I  S  K  G  A  Q  E  C  T  K  T  R  E

     TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGA
2929 -+---------+---------+---------+---------+------ 2976
     AAACTCTCCAAAGTCCTCTACACAATGTTCCGAATAGATCGATAAGCT
     F  E  R  F  Q  E  M  C  Y  K  A  Y  L  A  I  R

     CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT
2977 ---+---------+---------+---------+---------+---- 3024
     GTCGTACGGTTAGAGAAGTATTTAGAAAAGAGTTACTACGAACCGAGA
     Q  H  A  N  L  F  I  N  L  F  S  M  M  L  G  S

     GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG
3025 -----+---------+---------+---------+---------+-- 3072
     CCTTACGGTCTTGATGTTAGAAAACTACTGTAACGTATGTAAGCTTTC
     G  M  P  E  L  Q  S  F  D  D  I  A  Y  I  R  K
```

FIG 16 (contd)

```
       ACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG
3073   ---------+---------+---------+---------+---------+   3120
       TGGGATCGGAATCTATTTTGACTCGTTCTCCGAAACCTCATAAAGTAC
       T  L  A  L  D  K  T  E  Q  E  A  L  E  Y  F  M

       AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT
3121   ---------+---------+---------+---------+--------     3168
       TTTGTTTACTTACTACGTGTAGTACCACCGACCTGTTGTTTTTACCTA
       K  Q  M  N  D  A  H  H  G  G  W  T  T  K  M  D

       TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACT
3169   -+---------+---------+---------+---------+------     3216
       ACCTAGAAGGTGTGTTAATTTGTCGTACGTAACTTGACTTTCTATTGA
       W  I  F  H  T  I  K  Q  H  A  L  N  *

       GAGAAAATGAAAGCTCACTCTGGATTCCACACTGCACTGTTAATAACT
3217   ---+---------+---------+---------+---------+----     3264
       CTCTTTTACTTTCGAGTGAGACCTAAGGTGTGACGTGACAATTATTGA
```

FIG 16 (contd)

```
        CTCAGCAGGCAAAGACCGATTGCATAGGAATTGCACAATCCATGAACA
3265    -----+---------+---------+---------+---------+--    3312
        GAGTCGTCCGTTTCTGGCTAACGTATCCTTAACGTGTTAGGTACTTGT

        GCATTAGATTTACAGCAAGAACAGAAATAAAATACTATATAATTTAAA
3313    -------+---------+---------+---------+---------+    3360
        CGTAATCTAAATGTCGTTCTTGTCTTTATTTTATGATATATTAAATTT

        TAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTTC
3361    ---------+---------+---------+---------+--------    3408
        ATTACATTTGCGTTTGTCCCAAACTATCGTGAATTTGATCAAGTAAAG

        AAAA
3409    -+--   3412
        TTTT
```

FIG 16 (contd)

Alignment of human and bovine p110 cDNA nucleotide sequences.

Nucleotide Similarity: 96%

```
                  .         .         .         .         .
hum110   1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGCATCCACTTGATGCC  50
           ||||||||||||||||||||||||||||||||||||||||||||||||||
bov110   1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGCATCCACTTGATGCC  50

                  .         .         .         .         .
        51 CCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACTT 100
           ||||||||||||||| |||||||||||||||||||| |||||||||||||
        51 CCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTGACTT 100

                  .         .         .         .         .
       101 TAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTT 150
           |||||||||||||||||||||| ||| |||| ||||||||||||||||||
       101 TAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACTATTT 150

                  .         .         .         .         .
       151 AAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       151 AAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200
```

Figure 17

```
201 TTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAATTTTTTG 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 TTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAATTTTTTG 250

251 ATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTTTAAAA 300
    |||||||||||||||||||||| ||||||||||||||||| |||||||||
251 ATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCCTTTTAAAA 300

301 GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAAT 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 GTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAAT 350

351 TGGTTTTGCTATCGGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATC 400
    ||||||||||||||||||||||||||| ||||| ||||||||||||||||
351 TGGTTTTGCTATCGGCATGCCAGTGTGTGAATTCGATATGGTTAAAGATC 400

401 CTGAAGTACAGGACTTCCGAAGAAATATTCTTAATGTTTGTAAAGAAGCT 450
    | ||||||||||||||||||||||||||||| ||||||||||||||||||
401 CAGAAGTACAGGACTTCCGAAGAAATATTCTCAATGTTTGTAAAGAAGCT 450
```

FIG 17 (contd)

```
451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGAGCAATGTATGTCTA 500
    ||||||||||||||||||||||||||||||||||||||||||||||| ||
451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGAGCAATGTATGTTTA 500

501 TCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCACATATATAATA 550
    ||| ||| ||||||||||||||||||| ||||||||||||||||||||||
501 TCCTCCAAATGTAGAATCTTCACCAGAACTGCCAAAGCACATATATAATA 550

551 AATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 600
    ||||||||| ||| ||||||||||||||||||||||||||||||||||||
551 AATTGGATAAAGGGCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCA 600

601 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
    ||||||||||| ||||||||||||||||||||||||||||||||||||||
601 AATAATGACAAACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650

651 AGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGC 700
    ||||||||||||||||||||||||||||||||||||| ||||||||||||
651 AGAACAAGTAATTGCTGAAGCAATCAGGAAAAAAACTCGAAGTATGTTGC 700
```

FIG 17 (contd)

```
                  .         .         .         .         .
701 TATCATCTGAACAATTAAAACTCTGTGTTTTAGAATATCAGGCAAGTAC 750
    |||||||||||||| |||||||||||||||||||||||||||||||||| 
701 TATCATCTGAACAACTAAAACTCTGTGTTTTAGAATATCAGGCAAGTAT 750
                  .         .         .         .         .
751 ATTTTAAAAGTGTGTGGATGTGATGAATACTTCCTAGAAAAATATCCTCT 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 ATTTTAAAAGTGTGTGGATGTGATGAATACTTCCTAGAAAAATATCCTCT 800
                  .         .         .         .         .
801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850
    |||||||||||||||||||||||||||||||||||||||||||||||||
801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850
                  .         .         .         .         .
851 ATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 900
    |||||| | ||||||||||||||||||| |||||||||||||||||||||
851 ATTTGATGCTGATGGCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGAC 900
                  .         .         .         .         .
901 TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATA 950
    ||||||||||||||||| ||||||||||||||| |||||||||| |||||
901 TGTTTTACAATGCCATCATATTCCAGACGCATCTCCACAGCTACGCCATA 950
```

FIG 17 (contd)

```
                 .         .         .         .         .
 951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC 1000
     ||||||||||||||||||||||||||||||||||||||||||||| ||||
 951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCAC 1000
                 .         .         .         .         .
1001 TCAGAATAAAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC 1050
     |||||||||||||||||||||||||||| |||||| ||||||||||||||
1001 TCAGAATAAAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC 1050
                 .         .         .         .         .
1051 ATTGACAAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTT 1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1051 ATTGACAAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTT 1100
                 .         .         .         .         .
1101 ATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
     |||||| |||||||||||||||||||||||||||||||||||||||||||
1101 ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
                 .         .         .         .         .
1151 ATGAATGGCTGAATTATGATATATACATTCCTGATCTTCCTCGTGCTGCT 1200
     |||||||||||||||| |||||||||||||||||||||||||||||||||
1151 ATGAATGGCTGAATTACGATATATACATTCCTGATCTTCCTCGTGCTGCT 1200
```

FIG 17 (contd)

```
                    .         .         .         .         .
1201 CGACTTTGCCTTTCCATTTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGA 1250
     |||||||||||||||||||| |||||||||||||||||||||||||||||
1201 CGACTTTGCCTTTCCATTTGTTCTGTTAAAGGCCGAAAGGGTGCTAAAGA 1250

                    .         .         .         .         .
1251 GGAACACTGTCCATTGGCATGGGAAATATAAACTTGTTTGATTACACAG 1300
     |||||||||||||||||| |||||||||||||||||||||||||||||||
1251 GGAACACTGTCCATTGGCCTGGGAAATATAAACTTGTTTGATTACACAG 1300

                    .         .         .         .         .
1301 ACACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350
     | ||||||||||||||||||||||||||||||||||||||||||||||||
1301 ATACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350

                    .         .         .         .         .
1351 GGATTAGAAGATTTGCTGAACCCTATTGGTGTTACTGGATCAAATCCAAA 1400
     ||| ||||||||||||||||||||||||||||||||||||||||||||||
1351 GGACTAGAAGATTTGCTGAACCCTATTGGTGTTACTGGATCAAATCCAAA 1400

                    .         .         .         .         .
1401 TAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
     ||||||||||||||| ||||||||||||||||||||||||||||||||||
1401 TAAAGAAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
```

FIG 17 (contd)

```
                   .         .         .         .         .
1451 TAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA 1500
     ||||||| ||||||||||||||||||||||||||||||||||||||||||
1451 TAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA 1500
                   .         .         .         .         .
1501 TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACT 1550
     ||||| |||||||||||||| |||||||| ||||||||||||||||||||
1501 TCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTGAGTAACAGACT 1550
                   .         .         .         .         .
1551 AGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAA 1600
     ||||||||||||||||||||| |||||||| ||||||||||||  |||||
1551 AGCTAGAGACAATGAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAA 1600
                   .         .         .         .         .
1601 TTTCTACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTT 1650
     ||| ||||||||||||||| ||||||||||||||||| ||||||||||||
1601 TTTGTACACGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAGATTTT 1650
                   .         .         .         .         .
1651 CTATGGAGTCACAGACACTATTGTGTAACTATCCCCGAAATTCTACCCAA 1700
     || ||||| |||||||||||||||||||||||||||||||||||||||||
1651 CTGTGGAGCCACAGACACTATTGTGTAACTATCCCCGAAATTCTACCCAA 1700
```

FIG 17 (contd)

```
1701 ATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTAGCCCAGATGT 1750
     |||||||||||||||||||||||| ||||||||||||||||| |||||||
1701 ATTGCTTCTGTCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750

1751 ATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA 1800
     | ||||||||||||||||||||||||||||| ||||||||||||||||| 
1751 ACTGCTTGGTAAAAGATTGGCCTCCAATCAAGCCTGAACAGGCTATGGAG 1800

1801 CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCG 1850
     ||||||||||| ||||||||||||||||||||||||||||||||||||||
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTTCG 1850

1851 GTGCTTGGAAAAATATTTAACAGATGACAAACTTTCTCAGTATTTAATTC 1900
     |||||| |||||||||||||||||||||||||||||||||||  ||||||
1851 GTGCTTAGAAAAATATTTAACAGATGACAAACTTTCTCAGTACCTAATTC 1900

1901 AGCTAGTACAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGTG 1950
     ||||||||||||| |||||||||||||| |||||||||||| ||||||||
1901 AGCTAGTACAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTTGTG 1950
```

FIG 17 (contd)

```
1951 AGATTTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGGCACTTTTT 2000
     ||||||||||| || ||||| || |||||||||||||| || ||||||||
1951 AGATTTTTACTCAAAAAAGCGTTAACTAATCAAAGGATCGGTCACTTTTT 2000

2001 CTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTTAGCCAGAGGT 2050
     |||||||||||||||||||||||||||||||||||||||||| |||||||
2001 CTTTTGGCATTTAAAATCTGAGATGCACAATAAAACAGTTAGTCAGAGGT 2050

2051 TTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAG 2100
     ||||||||||||||||||||||||| |||||||||||||||||| |||||
2051 TTGGCCTGCTTTTGGAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAG 2100

2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACTTAACTGA 2150
     ||||| ||||||||||| ||||| |||||||||||||||||||| |||||
2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAAAGCTCATTAACTTGACTGA 2150

2151 CATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200
     |||||||||||| |||| ||||||||||||||||||||||||||||||||
2151 CATTCTCAAACAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200
```

FIG 17 (contd)

```
2201 TTTTAGTTGAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGC 2250
     ||||||||||||||||| |||||||||||||||||||||| || ||||||
2201 TTTTAGTTGAGCAAATGCGGCGACCAGATTTCATGGATGCTCTCCAGGGC 2250

2251 TTGCTGTCTCCTCTAAACCCTGCTCATCAACTAGGAAACCTCAGGCTTAA 2300
     || |||||||||||||||||||||||||| || ||||| ||||||||| |
2251 TTTCTGTCTCCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300

2301 AGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2301 AGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350

2351 AGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAGATCATC 2400
     |||||||||||||||||||||| ||||| |||||||||||||||||||||
2351 AGAACCCAGACATCATGTCAGAATTACTCTTTCAGAACAATGAGATCATC 2400

2401 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTAT 2450
     |||||||||||||||||||||||||||||||||||||| ||||| |||||
2401 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATTAT 2450
```

FIG 17 (contd)

```
2451 TCGTATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGT 2500
     ||| ||||||||||||||||||||||||||||||||||||||||||||||
2451 TCGCATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGT 2500

2501 TACCTTATGGTTGTCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTG 2550
     |||||||||| ||||||||||||||||||||||||||||||| ||||||
2501 TACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGACTTATCGAGGTG 2550

2551 GTGCGAAATTCTCACACTATTATGCAAATTCAGTGCAAAGGCGGCTTGAA 2600
     ||| |||||||||||||||| ||||| |||||||| ||||| ||| ||||
2551 GTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAAGGAGGCCTGAA 2600

2601 AGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGGCTCAAAGACA 2650
     ||||||||||||||| |||||||||||||| |||||||||||||||||||
2601 AGGTGCACTGCAGTTTAACAGCCACACACTCCATCAGTGGCTCAAAGACA 2650

2651 AGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA 2700
     ||||||| || |||||||||||||| ||||| ||  |||||||||| |||
2651 AGAACAAGGGGGAAATATATGATGCGGCCATCGATTTGTTTACACGATCA 2700
```

FIG 17 (contd)

```
2701 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA 2750
     ||||||||||| ||||| || |||||||||||||||||||||||||||||
2701 TGTGCTGGATATTGTGTTGCCACCTTCATTTTGGGAATTGGAGATCGTCA 2750

2751 CAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATT 2800
     ||||||||| |||||||| ||||| |||||||||||||||||||||||||
2751 CAATAGTAATATCATGGTTAAAGATGATGGACAACTGTTTCATATAGATT 2800

2801 TTGGACACTTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAA 2850
     ||||||||||||||||||||||||||||||||||||||||||||||||| 
2801 TTGGACACTTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAG 2850

2851 CGTGTGCCATTTGTTTTGACACAGGATTTCTTAATAGTGATTAGTAAAGG 2900
     || ||||| |||||||||||||| ||||||||||||||||||||||||||
2851 CGCGTGCCGTTTGTTTTGACACAAGATTTCTTAATAGTGATTAGTAAAGG 2900

2901 AGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTTCAGGAGATGT 2950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2901 AGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTTCAGGAGATGT 2950
```

FIG 17 (contd)

```
                   .         .         .         .         .
2951 GTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT 3000
     ||||||||||||||||||||||||| ||||||||||||||||||||||||
2951 GTTACAAGGCTTATCTAGCTATTCGGCAGCATGCCAATCTCTTCATAAAT 3000
                   .         .         .         .         .
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGA 3050
     |||||||||||||||||||||||||||||||||||||| |||||||||||
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGA 3050
                   .         .         .         .         .
3051 TGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAG 3100
     ||| |||||||||||||||||||||||||| |||||||||||||||||||
3051 TGATATTGCATACATTCGAAAGACCCTAGCTTTAGATAAAACTGAGCAAG 3100
                   .         .         .         .         .
3101 AGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGC 3150
     |||||||||||||||||||||||||||||||||||||||| |||||||||
3101 AGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCACACCATGGTGGC 3150
                   .         .         .         .         .
3151 TGGACAACAAAAATGGATTGGATCTTCCACACAATTAAACAGCATGCATT 3200
     |||||||||||||||||||||||||||||||||||||| |||||||| ||
3151 TGGACAACAAAAATGGATTGGATCTTCCACACAATTAAGCAGCATGCTTT 3200
```

FIG 17 (contd)

```
               .         .         .         .
3201  GAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA
      ||||||||
3201  GAACTGA.................................
```

FIG 17 (contd)

The alignment between human and bovine p110 proteins.

```
           10        20        30        40        50        60
h MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ
  ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
b MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLITIKHELFKEARKYPLHQ
           10        20        30        40        50        60

           70        80        90       100       110       120
h LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLKVIEPVGNREEKILNREIGFA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLKVIEPVGNREEKILNREIGFA
           70        80        90       100       110       120

          130       140       150       160       170       180
h IGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPHVESSPELPKH
  |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
b IGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPNVESSPELPKH
          130       140       150       160       170       180
```

Figure 18

```
      190       200       210       220       230       240
h IYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVIAEAIRKKTRSMLLSSEQLK
  ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
b IYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVIAEAIRKKTRSMLLSSEQLK
      190       200       210       220       230       240

      250       260       270       280       290       300
h LCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLKMMAKESLYSQLPMD
  |||||||||||||||||||||||||||||||||||||||||||||::|||||||||||||
b LCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLMLMAKESLYSQLPMD
      250       260       270       280       290       300

      310       320       330       340       350       360
h CFTMPSYSRRISTATPYMNGETSTKSLWVINRALRIKILCATYVNLNIRDIDKIYVRTGI
  |||||||||||||||||||||||||||||||:|||||||||||||:||||||||||||||
b CFTMPSYSRRISTATPYMNGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGI
      310       320       330       340       350       360
```

FIG 18 (contd)

```
               370       380       390       400       410       420
h YHGGEPLCDNVNTQRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSICSVKGRKGAKEEHC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b YHGGEPLCDNVNTQRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSICSVKGRKGAKEEHC
               370       380       390       400       410       420

               430       440       450       460       470       480
h PLAWGNINLFDYTDTLVSGKMALNLWPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b PLAWGNINLFDYTDTLVSGKMALNLWPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF
               430       440       450       460       470       480

               490       500       510       520       530       540
h SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTRDPL
  |||||||||||||||||||||||||||||||||||||||||||||||||||:||:|||||
b SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL
               490       500       510       520       530       540
```

FIG 18 (contd)

```
          550       560       570       580       590       600
h SEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAME
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b SEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAME
          550       560       570       580       590       600

          610       620       630       640       650       660
h LLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTN
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b LLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTN
          610       620       630       640       650       660

          670       680       690       700       710       720
h QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILK
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILK
          670       680       690       700       710       720
```

FIG 18 (contd)

```
          730       740       750       760·      770       780
h QERKDETQKVQMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLRLKECRIMSSAKRPLW
  ||:|||||||||||||||||||||||||||:|||||||||||||||:|||||||||||||
b QEKKDETQKVQMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEECRIMSSAKRPLW
          730       740       750       760       770       780

          790       800       810       820       830       840
h LNWENPDIMSELLFQNNEIIFKNGDDLRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLS
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b LNWENPDIMSELLFQNNEIIFKNGDDLRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLS
          790       800       810       820       830       840

          850       860       870       880       890       900
h IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRS
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRS
          850       860       870       880       890       900
```

FIG 18 (contd)

```
            910       920       930       940       950       960
h CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF
            910       920       930       940       950       960

            970       980       990      1000      1010      1020
h LIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b LIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA
            970       980       990      1000      1010      1020

           1030      1040      1050      1060      1070      1080
h YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXKITEKMKAHSG
  |||||||||||||||||||||||||||||||||||||||||||||||||
b YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNX
           1030      1040      1050      1060
```

FIG 18 (contd)

Figure 19. The predicted amino acid sequence of human p110 cDNA.

1	MPPRPSSGEL	WGIHLMPPRI	LVECLLPNGM	IVTLECLREA	TLVTIKHELF
51	KEARKYPLHQ	LLQDESSYIF	VSVTQEAERE	EFFDETRRLC	DLRLFQPFLK
101	VIEPVGNREE	KILNREIGFA	IGMPVCEFDM	VKDPEVQDFR	RNILNVCKEA
151	VDLRDLNSPH	SRAMYVYPPH	VESSPELPKH	IYNKLDRGQI	IVVIWVIVSP
201	NNDKQKYTLK	INHDCVPEQV	IAEAIRKKTR	SMLLSSEQLK	LCVLEYQGKY
251	ILKVCGCDEY	FLEKYPLSQY	KYIRSCIMLG	RMPNLKMMAK	ESLYSQLPMD
301	CFTMPSYSRR	ISTATPYMNG	ETSTKSLWVI	NRALRIKILC	ATYVNLNIRD
351	IDKIYVRTGI	YHGGEPLCDN	VNTQRVPCSN	PRWNEWLNYD	IYIPDLPRAA
401	RLCLSICSVK	GRKGAKEEHC	PLAWGNINLF	DYTDTLVSGK	MALNLWPVPH
451	GLEDLLNPIG	VTGSNPNKET	PCLELEFDWF	SSVVKFPDMS	VIEEHANWSV

```
501   SREAGFSYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF
551   LWSHRHYCVT IPEILPKLLL SVKWNSRDEV AQMYCLVKDW PPIKPEQAME
601   LLDCNYPDPM VRGFAVRCLE KYLTDDKLSQ YLIQLVQVLK YEQYLDNLLV
651   RFLLKKALTN QRIGHFFFWH LKSEMHNKTV SQRFGLLLES YCRACGMYLK
701   HLNRQVEAME KLINLTDILK QERKDETQKV QMKFLVEQMR RPDFMDALQG
751   LLSPLNPAHQ LGNLRLKECR IMSSAKRPLW LNWENPDIMS ELLFQNNEII
801   FKNGDDLRQD MLTLQIIRIM ENIWQNQGLD LRMLPYGCLS IGDCVGLIEV
851   VRNSHTIMQI QCKGGLKGAL QFNSHTLHQW LKDKNKGEIY DAAIDLFTRS
901   CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHFLDH KKKKFGYKRE
951   RVPFVLTQDF LIVISKGAQE CTKTREFERF QEMCYKAYLA IRQHANLFIN
1001  LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM KQMNDAHHGG
1051  WTTKMDWIFH TIKQHALN*
```

FIG 19 (contd)

The human PITR-c partial cDNA nucleotide and deduced amino acid sequence.

```
1    GGAGACGACTTGCGACAGGATCAACTTATTCTTCAAATCATTTCACTC
     GlyAspAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu

49   ATGGACAAGCTGTTACGGAAAGAAAATCTGGACTTGAAATTGACACCT
     MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro

97   TATAAGGTGTTAGCCACCAGTACAAAACATGGCTTCATGCAGtTTATC
     TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle

145  CAGTCAGTtCCTGTGGCTGAaGTTCTTGATACAGAGGGAAGCATTCAG
     GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln

193  AACTTTTTTAGAAAATATGCACCAAGTGAGAATGGGCCAAATGGGATT
     AsnPhePheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle

241  AGTGCTGAGGTCATGGACACTtACGTTAAAAGCTGTGCTGGATATTGC
     SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys

289  GTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTT
     ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu
```

Figure 20

337 TTGCTAACcAAAACAGGCAAACTCTTCCACATCGATTTCGGcCAC
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis

FIG 20 (contd)

The human PITR-f partial cDNA nucleotide and deduced amino acid sequence.

```
  1  GGGGATGACTTACGGCAGGACATGCTAACGCTGCAGATGATTCGCATC
     GlyAspAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

 49  ATGAGCAAGATCTGGGTCCAGGAGGGGCTGGACATGCGCATGGTCATC
     MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

 97  TTCCGCTGCTTCTCCACCGGCCGGGGCAGAGGGATGGTGGAGATGATC
     PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145  CCTAATGCTGAGACCCTGCGTAAGATCCAGGTGGAGCATGGGGTGACc
     ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193  GGCTCGTTCAAGGACCGGCCCCTGGCAGACCGGCTGCAGAAACACAAC
     GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241  CCTGGGGAGGACGAGTATGAGAAGGCTGTGGaGAACTTTATCTACTCC
     ProGlyGluAspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289  TGCGCTGGCTGCTGCGTGGCCACGTACGTCTTGGGCATCTGTGACCga
     CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg
```

Figure 21

337 CATAATGACAACATCATGCTGAAGACCACTGGTCACATGTTCCACATC
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC
AspPheGly

FIG 21 (contd)

ALIGNMENT OF HUMAN P110, HUMAN PI-3 KINASE RELATED GENES PITR-C AND PITR-F AND YEAST PI-3 KINASE VPS34.

In upper case are shown amino acids that are conserved in 3 or more of the proteins. Underlined are the residues involved in ATP binding.

```
          1                                                50
vps34     GDDLRQDqLvvQIIslMnellknEnvDLkLtPYkiLaTGpqeGaIEfIpN
PITR-c    GDDLRQDqLiLQIIslMdkllrkEnLDLkLtPYkvLaTstkhGFmqfIqs
hump110   GDDLRQDmLtLQIIriMeniwqnqgLDLrMlPYgcLsiGdcvGLIEvVrN
PITR-f    GDDLRQDmLtLQmIriMskiwvqEgLDMrMviFrcFsTGrgrGMVEmIpN
Consensus GDDLRQD-L-LQII--M------E-LDL---PY--L-TG---G-IE-I-N

          51                                              100
vps34     dtlasilskyhGIlGy......LklhypdeNatlgVqgwvlDnFVkSCA
PITR-c    vpvaevldtegsIqnf......FrkYapseNgpngIsaevmDtYVkSCA
hump110   shtimqiqckgGlkGalqfnshtLhqWlkdkNkge.IydaaiDlFtrSCA
PITR-f    aetlrkiqvehGVtGs..fkdrpLadrlqkhNpgedeyekavEnFIySCA
Consensus -----------GI-G--------L-------N----I-----D-FV-SCA
```

Figure 22

```
          101                              133
vps34     GYCViTYILGVGDRHlDNlLvtpdGhFFHaDFG
PITR-c    GYCViTYILGVGDRHlDNlLltktGkLFHIDFG
hump110   GYCVaTFILGIGDRHnsNiMvkddGqLFHIDFG
PITR-f    GCCVaTYVLGIcDRHnDNiMlkttGhMFHIDFG
Consensus GYCV-TYILG-GDRH-DN------G-LFHIDFG
```

FIG 22 (contd)

Figure 23 A

MAPPING THE P85 BINDING SITE ON P110

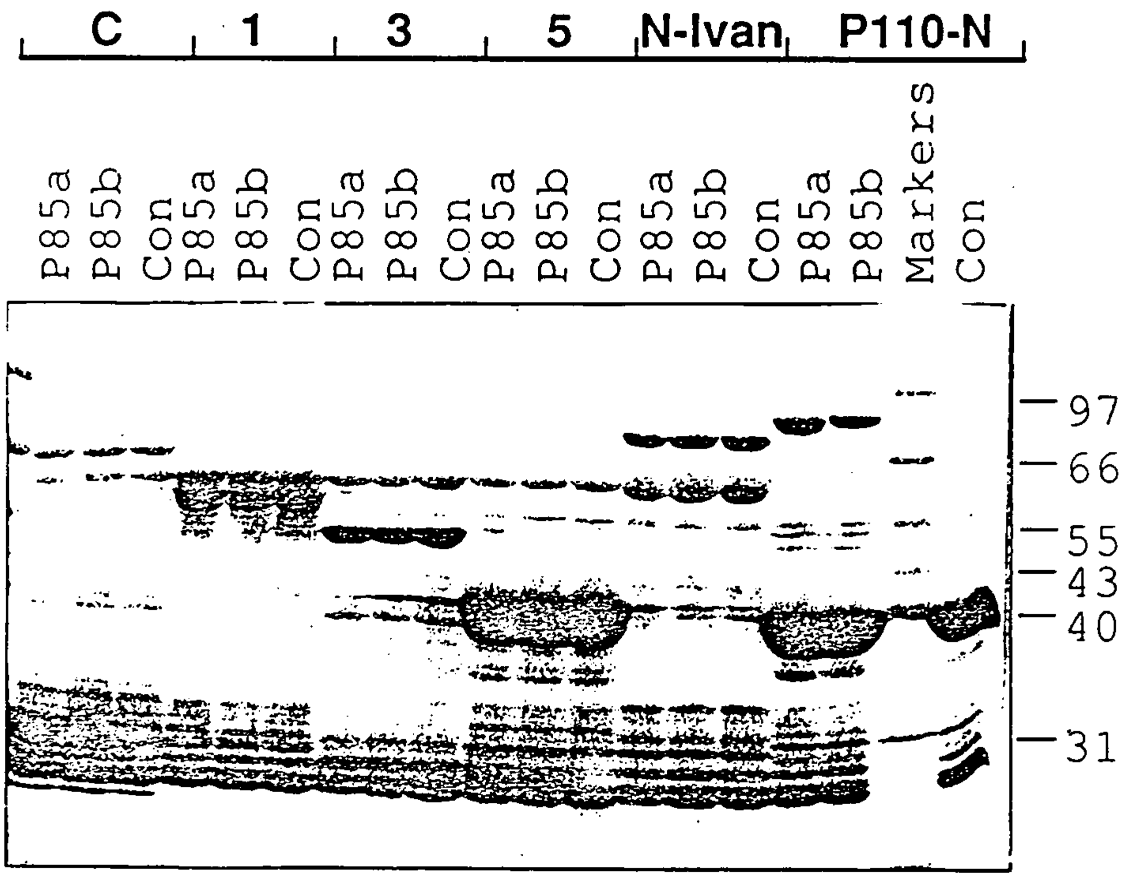


Figure 23 B

Locating the P85 binding site on P110

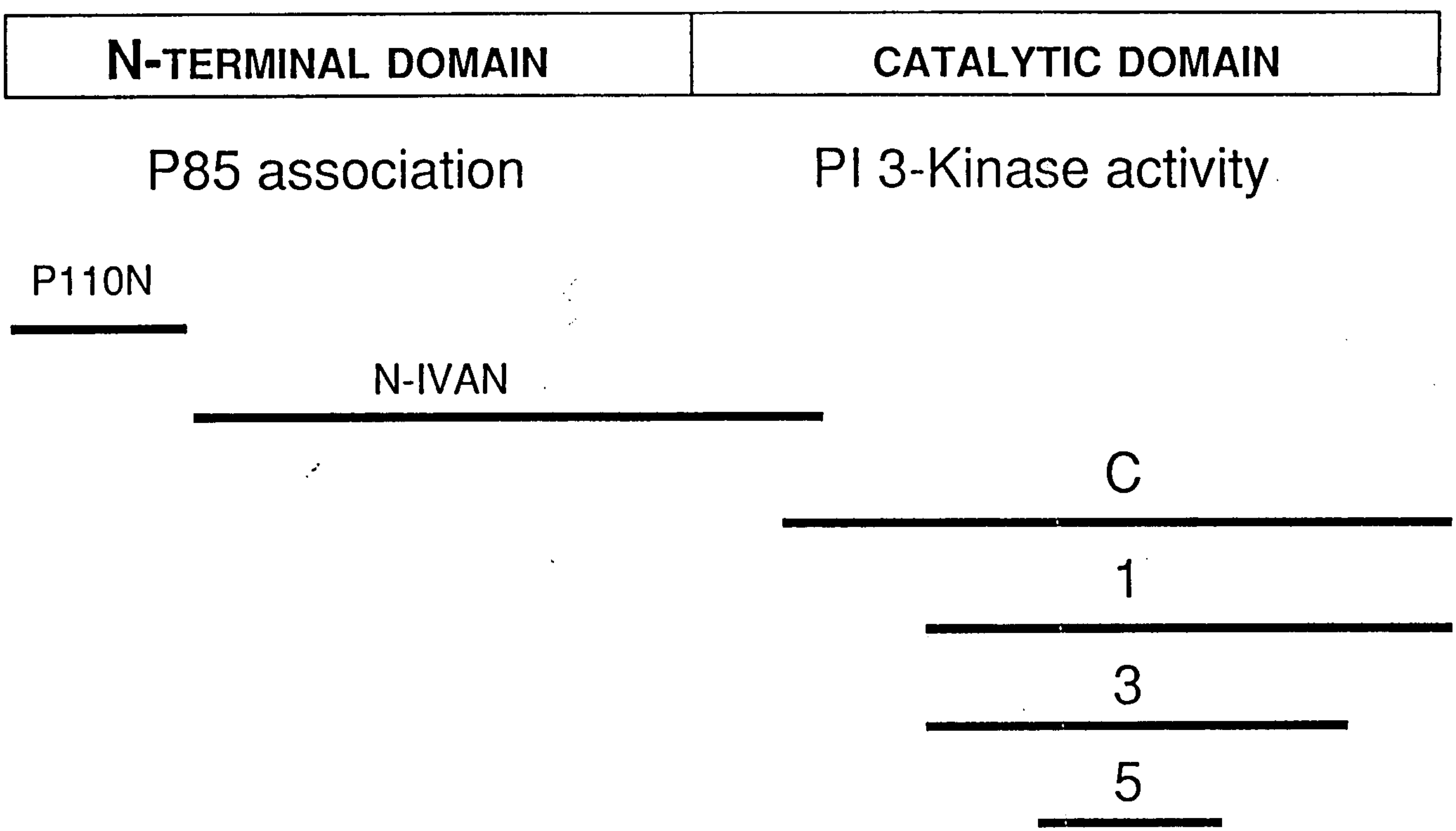


Figure 24

Mapping of the P85 Binding Site on P110

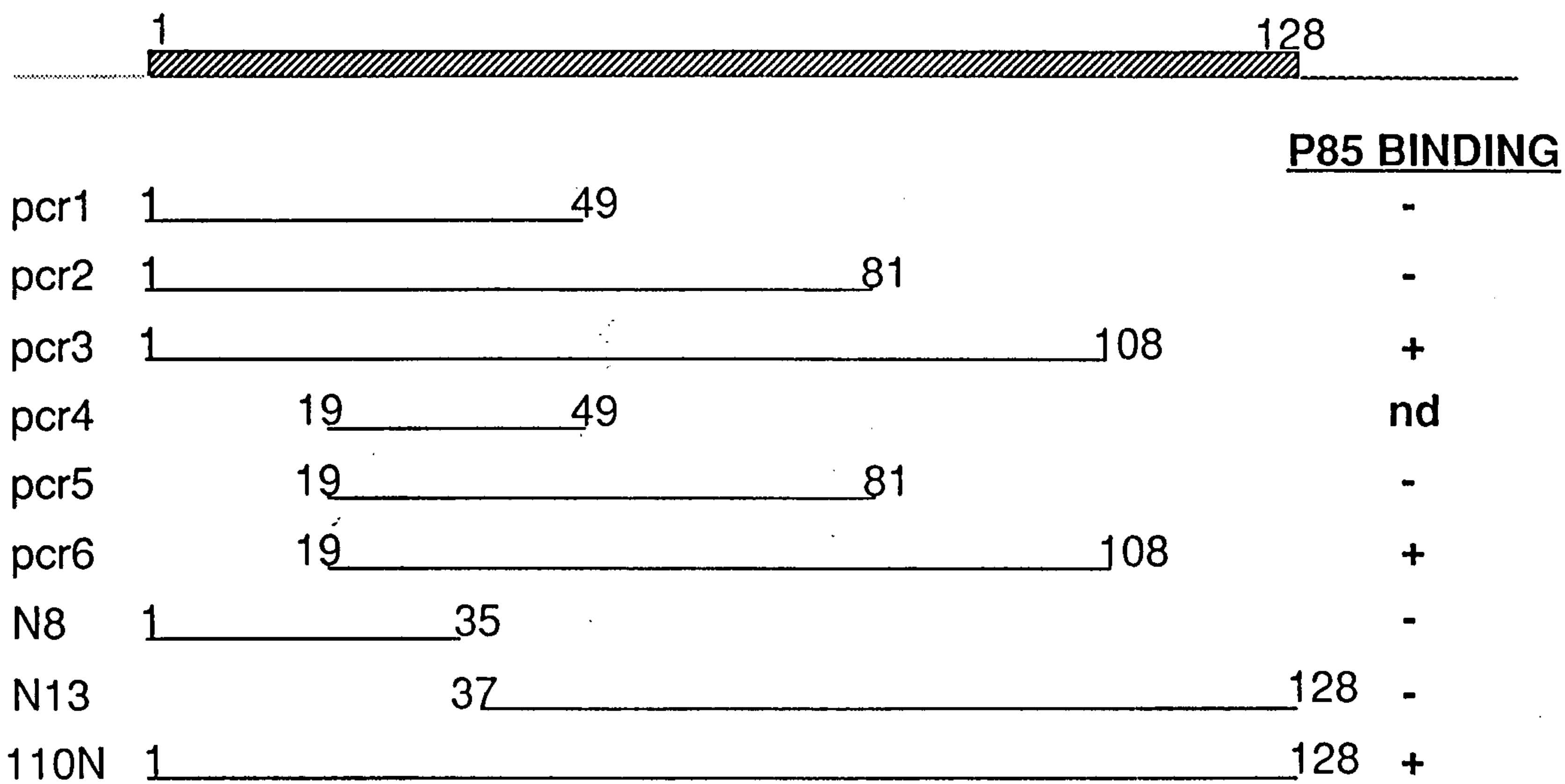


Figure 25 A

MAPPING THE P85 BINDING SITE ON P110

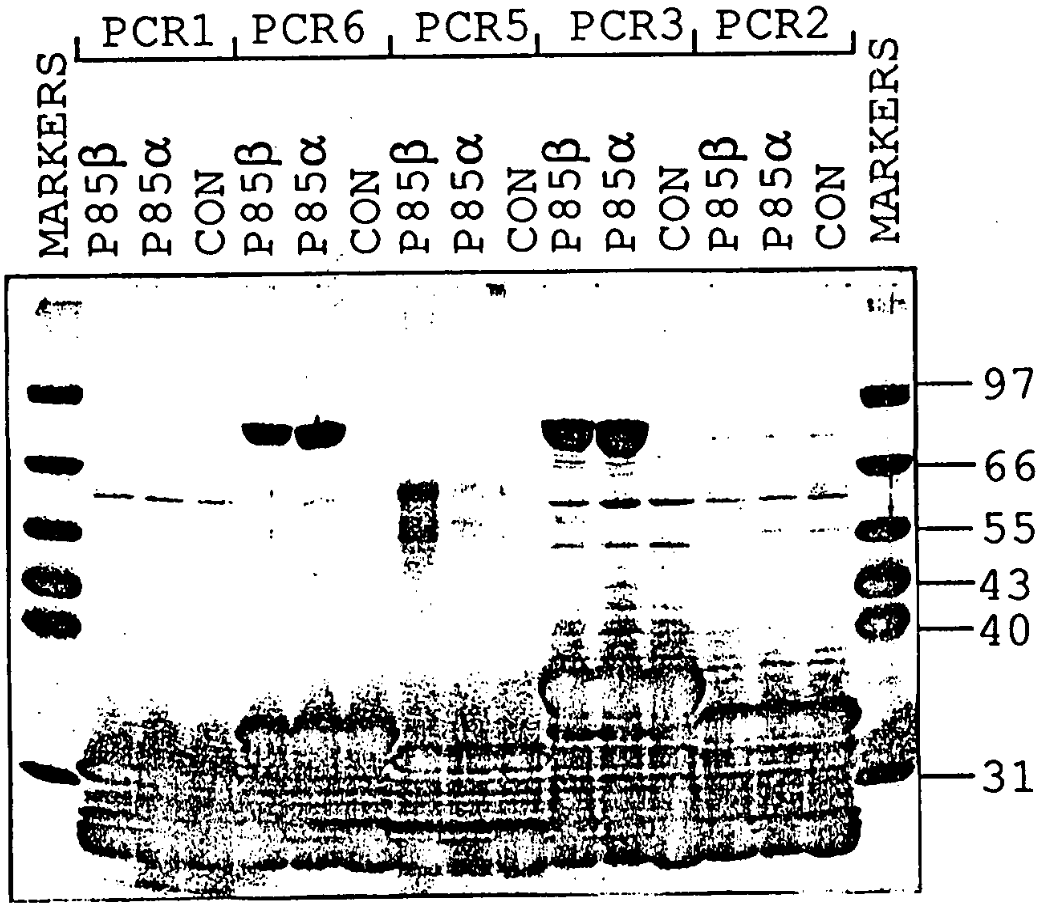


Figure 25 B

MAPPING THE P85 BINDING SITEON P110 (2)